- protein search, using sw model

OM protein

Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

US-09-843-250-2 2408

Perfect score:

Sequence:

Sequence 78, Appl Sequence 9, Appl Sequence 9, Appl Sequence 18, Appl Sequence 11, Appl Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 44, Appl Sequence 45, Appl Sequence 45, Appl Sequence 46, A Sequence 5603, Ap Sequence 12181, A Sequence 12995, A Sequence 46, Appl Sequence 1362, Ap Sequence 45, A Sequence 246, A Sequence 17, A Sequence 17, A Sequence 17, A 9 US-10-047-542-78 9 US-09-924-097-15 10 US-09-776-490-9 11 US-09-776-491-18 11 US-09-776-491-18 12 US-09-776-491-18 13 US-09-776-491-11 14 US-09-776-491-11 15 US-09-776-491-10 16 US-09-776-491-10 17 US-09-776-491-10 18 US-09-776-491-10 18 US-09-776-491-10 18 US-09-776-491-45 18 US-09-776-491-45 18 US-09-776-491-45 18 US-09-776-491-45 18 US-09-776-491-45 18 US-09-776-491-17 18 US-09-776-491-17 18 US-09-776-491-17 18 US-09-776-491-17 18 US-09-776-491-45 18 US-09-815-742-12181 01110011001100 January 27, 2003, 09:02:32 ; search time 7 Seconds (without alignments) 1294.310 Million cell updates/sec 1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 122226 5.1.3 Compugen Ltd. Total number of hits satisfying chosen parameters: 122226 seqs, 20178551 residues GenCore version Copyright (c) 1993 - 2003

ALIGNMENTS

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROMER: 05/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/2019,078

PRIOR APPLICATION NUMBER: 60/200,848

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,537

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308 Sequence 10253, Application US/09815242 Patent No. US20020061569A1 BENEAL INFORMATION: APPLICANT: Haselbeck, Robert NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FastSEQ for Windows Version APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T. ; ORGANISM: Escherichia coli US-09-815-242-10253 RESULT 1 US-09-815-242-10253

/cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

Published_Applications_AA:*

Database :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 10253, A	Sequence 6140, Ap				Sequence 19,	Sequence 20, A	Sequence 20, A	Sequence 21, App.	Sequence 21, App.		Sequence 12, App	Sequence 12, Appl	14,	14,	Sequence 13, A	15,	13,	Sequence 15, Appl
(I	US-09-815-242-10253	US-09-738-626-6140	US-09-815-242-11692	US-09-815-242-5097	US-09-776-490-19	US-09-776-491-19	US-09-776-490-20	US-09-776-491-20	US-09-776-490-21	US-09-776-491-21	US-08-976-063C-4	US-09-776-490-12	US-09-776-491-12	US-09-776-490-14	US-09-776-491-14	US-09-776-490-13	US-09-776-490-15	US-09-776-491-13	US-09-776-491-15
DB	10	6	10	10	10	10	10	10	10			10		10	10	10	10	10	10
Query Match Length DB	453	490	385	424	35	35	35	35	35	35	354	35	35	35	35	35	35	35	35
Query Match	30.6	15.6	15.6	14.1	7.7	7.7	7.2	7.2	7.0	7.0	4.9	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5
Score	736	376	375.5	340.5	185	185	174	174	168	168	118.5	110	110	109	109	108	108	108	108
Result No.	1	2	m	4	Ŋ	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19

Length 453;

Score 736; DB 10; Pred. No. 1.1e-57;

30.6%; 36.4%;

Query Match Best Local Similarity

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Query Match
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                                                                                           VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                       RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP 198
                                                                                                                                                                                                                                                                                 --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY 292
                                                                                                                                                                                                                                                                                                                257 QDGHGSGFFFFTEKPDANVWV--DGAVSSYYRETYAE------AEQRLGEVRALRL 303
                                                                                                                                                                                                                                                                                                                                             RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTV 352
                                                                                                                                                                                                                                                                                                                                                                                                           GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS 412
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   Gaps
                              IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                             Gaps
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                                                                                                                                                                                                                     199 AENFVGDAYHVGWTHASSL------RSGESIFSSLAGNAALP------
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 64; Mismatches 174; Indels
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Pred. No. 1.3e-25;
66; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK 453
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CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: JD 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Corynebacterium glutamicum
US-09-738-626-6140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.6%;
Best Local Similarity 26.3%;
Matches 118; Conservative 6
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HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
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SENOH, AKIHIRO
IKEDA, MASATO
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6140
Matches 165; Conservative
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138 VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWK 196
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                                                                                                                                                                                                                                                                                                                                                                                 APAENFVGDAYHVGWTH----ASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGM 250
                                                                                                                                                                                                                                                                                                                                                                                                                            207 LQTEN-GADGYHVSSTHWNYAATTSRRGTGESANETKAMDAGTWGKQGGGYFSYPYGHML 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPNNSML-T 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 --LWMWWGNPEDRPLF-----ERRDEFKKEFGEEKGEFWGASRNLCLYPNVYLMDQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 CSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWESDDNDNMET 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO---KTYQASAFPWNDM--TRGLGHQVQG----PNEVAKGLGMNEVLSSGARTEDEGLY 426
                                                                                                    80 VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKD-LYGESLNKK-CLGLKE 137
27 IFTDPEIFELEMRHIFEGNWIYLAHESQIPNAGDYFTTYIGRQPIMITRSKDGTLNCLIN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 FSSQIRHIRPISVDQTEVTIYCIAPKGESAEARANRIRQYEDFFNATGMATPDDLEEFRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 11692
LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RAYQAHVSSSNWAEFEHASST 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 PIQHGFWHELMQEAVNKQSIKEKELADDT 455
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PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/23,625
PRIOR PELLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11692, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-03-2
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15.6%; Score 375.5; DB 10; Length 385;

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211

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142 ESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAE 200
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                                                                                                                                                                                                                                                                                                               200 NGV-DAYHLPFAHKRYLEYLNTL-------GIDPESHKRHGRG-EALGNGHALI 244
                                                                                                                                                                                                                                                                                                                                                                                  ----ADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPN--- 303
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                                                                             85 GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKC---LGLKEVARV 141
                                                                                                                                                                                                                                                                                                                                                                                                                               245 ISGPPSTGRPIAYWSPLFPEALKPSIAAKFERLVERFGQARAEDIAHTNKSLFIFPNLVI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 NSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWESDDN 363
       24 ELHRRELHEIFDDSWLYAAHLSELREPGDFITRDVGGRNLIIQRRADGEPAVYLNACAHR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 DNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::1: : | |||:| | |||:| 363 EILESCQ---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREW 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: No. US20010012886Alth Carolina COUNTRY: USA
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APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09776490 Patent No. US20010012886A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 919-881-3140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 FDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAENFVGDAYHVG 210
                                                                                                                                                                                                                                                                                                     182 VVHWNYASTMSRRNYEA----EGTHTVDANGWSKSLGGGYGFDNGHMLLW-----TR 229
                                                                                                                                                                        94 GNAKGFVCSYHGWGFGSNGELQSVPFEK-DLYGESL-NKKCLGLKEVARVESFHGFIYGC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 DLVPELMAFGGAKQERLNKEIGDVRA-RIYRSHLNCTVFPNNSML-TCSGVFKVWNPIDA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                           IFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEA 93
                                                                                                                         IFEGNWVFLAHESQIPQPGDYYTLTLGRQPVIITRDKKNELHALINSCAHRGAMLCRRKT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
                                                                                                                                                                                                                                                                                                                                                                        ---WTHASSL--RSGESIFSSLAGNAALPPEGAGLQMTSKYG--SGMGVLWDGYSGVHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 NTTEV--WTYAIV-EKDMPEDLKRRLADSVQRTVGPAGFWESDDNDNMETASQNG 373
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                            Indels
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APPLICANT: Xu, H. Howard
TITLE OF INVERTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
ed. No. 1e-25;
Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.1%; Score 340.5; DB 10; Best Local Similarity 27.3%; Pred. No. 1.5e-22; Matches 114; Conservative 71; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
RURENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/225,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-22
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     Pred.
Best Local Similarity 31.0%; Pr
Matches 110; Conservative 58;
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Carr, Grant J.
Yamamoto, Robert T.
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Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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APPLICANT:
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GENERAL INFORMATION:
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Matches
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                                                      Length 35;
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                                                                                               1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
                                                      Score 185; DB 10;
Pred. No. 2.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%; Score 185; DB 10; 94.3%; Pred. No. 2.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Charlotte
STATE: No. US20010013135Alth Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MUTRAY
REGISTRATION NUMBER: 32,943
TELECOMMUNICATION INFORMATION:
TELECHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                     1 NVCRHRGKTLVSVEAGNAKGPVCSYHGWGFGSNGK 35
                                                                                         1; Mismatches
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FILING DATE: 02-Feb-2001
CLASSIFICATION: <UNKNOWN>
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                            Sequence 19, Application US/09776491
Patent No. US20010013135A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Briggs, Steven P. Johal, Gurmukh S. Gray, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                      7.78;
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 65
                                                                                           33; Conservative
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Matches 33; Conservative
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                                                      Query Match
Best Local Similarity
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US-09-776-490-19
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US-09-776-491-19
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                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
MIMMER OF SEOUENCES: 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <unimage columns of the columns of t
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CITY: Charlotte
STATE: No. US20010013135Alth Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                               PARK & GIBSON
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APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-776-490-20
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
CITY: Charlotte
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TELEPHONE: 919-881-3140
TELERAX: 919-881-3175
TELEX: 575102
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MEDIUM TYPE: Floppy disk
APPLICANT: Briggs, Steven P. Johal, Gurmukh S. Gray, John
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
                                                                                                                                                                                                                                                          Score 168; DB 10;
Pred. No. 9.3e-09;
3; Mismatches 4;
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80.0%; Pred. No. 9.3e-09;
live 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: No. US20010013135Alth Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                             79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/810,009
                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-776-490-21
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SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-776-491-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/09776491
Patent No. US20010013135A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-MAR-1997
                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Briggs, Steven P. Johal, Gurmukh S. Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                      TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 35 amino acids
TELEFAX: 919-881-3175
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                                                                                                                                                                                                                                                          7.0%;
80.0%;
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 28; Conservative
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Best Local Simi
Matches 28;
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               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTZER, PARK & GIBSON
STREET P.O. Drawer 34009
CITY: Charlotte
STATE: No. US20010012886A1th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 174; DB 10;
85.7%; Pred. No. 2.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                APPLICATION NUMBER: US 08/810,009
RILING DATE: 04-74R-1997
ATORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/776, 491
FILING DATE: 02-Feb-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: CURNOWN>
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
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REFERENCE/DOCKET NUMBER: 5718-4
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
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NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                    TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Briggs, Steven P. Johal, Gurmukh S. Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                               TELEX: 575102 INFORMATION FOR SEQ ID NO: 20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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Best Local Similarity
Matches 30; Conserv
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CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
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Pred. No. 0.0013;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                           PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NO. US20010012886Alth Carolina COUNTRY: USA
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APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 5718-4
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFRAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-776-490-12
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US-09-776-491-12
Sequence 12, Application US/09776491
Patent No. US20010013135A1
GENERAL INFORMATION:
HOPORMATION:
HOPORMATION:
GENERAL GORDER
HOPORMATION:
HOPORMATION:
GENERAL GORDER
HOPORMATION:
HOPORM
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ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
CITY: Charlotte
                                                                                           Sequence 12, Application US/09776490 Patent No. US20010012886A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 35 amino acids
                                                                                                                                                                                            APPLICANT: Briggs, Steven
Johal, Gurmukh
Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 575102
INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                     APPLICANT: Alexander Steinbuchel; Horst Priefert; Jurgen Rabenhorst
TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF
TITLE OF INVENTION: CONFERYL ALCOHOL, CONFERYLALDEHYDE, FERULIC ACID, VANILLIN ,
TITLE OF INVENTION: ACID AND THEIR USE
NUMBER OF SEQUENCES: 42
OORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 DNLM-DLTHETYVHASSIGOKEIDEAPVSTRVEGDTVITSRYMDNVMAPPFWRAALRGNG 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SGESIFSS-LAGNAALPP-----EGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage COMPUTER: HP VECTRA OPERATING SYSTEM: DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9%; Score 118.5; DB 1; 23.2%; Pred. No. 0.0065; tive 40; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: SPRUNG KRAMER SCHAEFER & BRISCOE 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 196 49 655.1 (Germany)
FILING DATE: 29-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9998-CAO
TELECOMMUICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/976,063C
FILING DATE: 21-NOV-1997
                                                                                                                                                                               Sequence 4, Application US/08976063C Publication No. US20020182697A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 ENFVGDAYHVGWTHASSLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 354 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 660 Whit
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10591-5144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                      RESULT 11
US-08-976-063C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-976-063C-4
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Matches
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 52.9°
Matches 18; Conservative
                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-776-491-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <unversely-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 110; DB 10;
52.9%; Pred. No. 0.0013;
tive 4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. US20010012886A1th Carolina
CITY: Charlotte
STATE: No. US20010013135Alth Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION UNDER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09776490
Patent No. US20010012886A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Briggs, Steven P. Johal, Gurmukh S. Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12:
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                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 18; Conserv
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US-09-776-490-14
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Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 35;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                               4.5%; Score 109; DB 10;
52.9%; Pred. No. 0.0016;
tive 3; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREFT: P.O. Drawer 34009
CITY: Charlotte
STATE: No. US20010013135Alth Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NQCRHRGMRICRADGGNAKSPTCSYHGWAYDSAG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
NAME: Spruill, W. Murray
REGIESTATION UNBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPAN: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-776-490-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09776491
Patent No. US20010013135A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briggs, Steven P. Johal, Gurmukh S. Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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US-09-776-491-14

ó 0; Gaps Query Match
4.5%; Score 109; DB 10; Length 35;
Best Local Similarity 52.9%; Pred. No. 0.0016;
Matches 18; Conservative 3; Mismatches 13; Indels

Dp δλ

Search completed: January 27, 2003, 09:20:54 Job time : 8 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 27, 2003, 08:56:07; Search time 10.1667 Seconds (without alignments) 1299.432 Million cell updates/sec Run on:

US-09-843-250-2 2408 1 MNYNNKILVSESGLSQKHLI......AEFEHASSTWHTELTKTTDR 449 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:* Database

1: /cgg_2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/pcTuS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Sequence 6, Appli Sequence 16, Appli Sequence 2, Appli Sequence 8, Appli Sequence 27, Appli Sequence 27, Appli Sequence 7, Appli	7,
US-09-036-987A-6 US-09-370-700-6 US-09-370-700-6 US-08-810-009-16 US-08-570-311-8 US-08-570-311-27 US-08-570-311-27 US-08-905-817-2 US-09-55-3-427-7 US-09-55-3-427-7 US-09-55-3-427-7 US-09-55-3-427-7 US-09-627-53-96-7	US-09-276-400-7 US-09-448-076-7
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944 993 993 993 991 990 990 990 990 990 990	90.5
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ALIGNMENTS

RESULT Sequence of the control of th	RESULT 1 US-09-004-393B-4 Sequence 4, Application US/09004393B Sequence 4, Application US/09004393B Patent No. 6310271 Settle No. 6310271 APPLICANT: Hanson D., Andrew APPLICANT: Hanson D., Andrew APPLICANT: Burnet, Michael TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and TITLE OF INVENTION: Polynucleotides CURRENT FILING DATE: 1998-01-08 FRICE REFERENCE: 1998-01-0
٥y	11 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
QQ	
Οy	71 DGSIRAFLNVCRHRCKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
qa	: ::: :
δλ	131 KCLGLKEVARVESFHGFIYGCFDQBAPPLMDYLGDAAWYLEPMFKHSGGLE 181
qq	: :
Qy	182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213

9

275 F-----PMECNWKVFCDNYLDSSYHVPYAH 299 Sequence 2, Application US/09004393B; Patent No. 631021 ; GENERAL INFORMATION: ; APPLICANT: Hanson D., Andrew RESULT 2 US-09-004-393B-2 g

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7.7%;
ilarity 94.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                           35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 amino acids
                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-810-009-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 33; Conserv
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                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                 7;
                              TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and TITLE OF INVENTION: Plants Transformed Therewith FILE REPERBNE: UF-105 CURRENT APPLICATION NUMBER: US/09/004,393B CURRENT FILING DATE: 1998-01-08 PRIOR PAPLICATION NUMBER: 60/035,147 PRIOR PAPLING DATE: 1997-01-08 SOFTWARE: Patentin Ver. 2.0 SEC ID NO 2 LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 SILACGSGKKSCFVCPYHGWYYGMDGSLAKASKAKP--EQNLDPKELGLVPL-KVAVWGP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                      27 FQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADBRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                         Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     Query Match 9.3%; Score 223; DB 4;
Best Local Similarity 30.1%; Pred. No. 5.7e-13;
Matches 58; Conservative 38; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Rathinasabapathi, Bala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: SFULIL, W. MURTEN,
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                        ; ORGANISM: Spinacia oleracea
US-09-004-393B-2
                   Burnet, Michael
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280 NYLDSSYHVPYAH 292
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US-08-810-009-19
APPLICANT:
                                                                                                                                                                                                                                                                       TYPE: PRT
                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESS:
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Length 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: US-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 919-881-3175
  Score 185; DB 4;
Pred, No. 5.2e-11;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 174; DB 4; ilarity 85.7%; Pred. No. 5.8e-10; Conservative 2; Mismatches 3
                                                                                             79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                   1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
GITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    US-08-810-009-20; Sequence 20, Application US/08810009; Sequence 10, Application US/08810009; Detent No. 6211437; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Maigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1506/CIP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-0CT-1996
PRIOR APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-UN-1994
ATTORNEY, AGENT INFORMATION:
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US-08-810-009-12
S-64-00-6-12, Application US/08810009
Patent No. 621447
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 20.3
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 379 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                   FILING DATE
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Sequence 21, Application US/08810009

Patent No. 6211437

GENERAL INPORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITT C CHARILOLLE
COUNTRY: No. 6211437th Carolina
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin 1.20/m2.20
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NO. 6117670artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: U.C. COUNTRY: U.S. ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09028934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOC AND SOPPHARED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEBEAX: 919-881-3175
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amin.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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US-09-028-934-36
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Matches
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62 PVVMERYCSHLGASL-----AKGKVVEGCIQCPFHNWRYDSTGACSHVP-----GHS 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 QSLRFAYETTTSVL----RII------ENFY-DAQHAAPVHQLPISAFELKLFDESS 206
                                                                                                                                                                                                                                                                                                  74 IRAFLNVCRHRGKTLVSVEAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGES 127
                                                                                                                                                                                                                                                                                                                                                                                                                                              128 LNKKCLGLKEVARVESF------HGFIYGCFDQEAP----PLMDYLGDAAWY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 LEPMFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGE-SIF---S 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 SLAGNAALPPE----GAGLQM-TSKYGSGMGVL--------WDGYSGVHSADLV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 PELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 -----GCIMTVSLD---GDVKYRL----LQCV---------TPVDKEETVM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 WTYAIVEKDMPEDLKRRLADSV---QRTVGPAGF----WESDDNDNMETASQNGKKYQSR 379
                                                                                 Gaps
                                                                                                                                                                                                 20 IHGDEELFQ-----HELKTIFARNW-LFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 PPPGQEALARDGAWFGAGIDFHVDRYFGPLGVISRTLGLSMSRMQLHFDGYPG-----
   Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 DSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSN 428
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-----KYRAFYRRWVNKVALEN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 HMLLAIKKG -- DGVVRSAANFILYGLQTWAAAGYDVAIWNSMKAD
   DB 3;
                                                                         54; Mismatches 149;
4.7%; Score 112.5; DB 20.3%; Pred. No. 0.017;
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26;

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-------LDPSRPGLEVFQ------VHENSNSPYGLSFRDAKTGKII 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/09311626B
; Patent No. 6399347
                                                                          REFERENCE DOCKET UNMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus licheniformis
                                     NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Jorgensen, Per Lina
                   ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                 35 amino acids
                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                       amino acid
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      US-08-810-009-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-311-626B-4
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LENGTH: 622
                                                                                                                                                                                                                                 LENGTH:
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GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.

APPLICANT: Johal, Gurmukh S.

APPLICANT: Johal, Gurmukh S.

APPLICANT: Johal, Gurmukh S.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING

TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ball, Selfzer, Park & GIBSON

STREET: P.O. Drawer 34009

CITY: Charlotte

STATE: No. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                 APPLICANT: Gray, John TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110; DB 4; Length 35;
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                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00077;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                      ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/810,009 FILLING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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Patent No. 6211437
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Spruil, W. Murray
REGIGSTRATION NUMBER: 32,943
REFRENCE/COCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
APPLICANT: Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 52.9
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                 28234
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US-08-810-009-14
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84 RGKTLVSVEAG--NAKGFVCS-----YHGWGFGSNGELQSVPFEK------DLYG 125 245 KGKVIGNANADYRNAQGRILSGPEYLTVFKG---DTGAELTTVNYEPARGNVADWGDSYG 301 162 YLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGE 221 359 YAGQG-----NHSLSVADVDGDGKDEIIYGAMAVDHDGKG-LYSTGWGHGDAMHTGN 409 222 SIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERL- 280 Query Match 4.5%; Score 109; DB 4; Length 622; Best Local Similarity 21.7%; Pred. No. 0.078; Matches 92; Conservative 50; Mismatches 130; Indels 152; Gaps 126 ESLNKKCLGL------CFDQEAPPLMD 161 Gaps APPLICANT: Schoort, Kirk
APPLICANT: Andersen, Lene No. 6399347boe
APPLICANT: Andersen, Lene No. 6399347boe
APPLICANT: Schulbin, Martin
APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
CURRENT APPLICATION NOWBER: US/09/311,626B
CURRENT FILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-01
PRIOR APPLICATION NUMBER: 60/08/98
PRIOR APPLICATION NUMBER: 60/08/4,358
PRIOR PILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0 ; 0 Length 35; Indels 13; Query Match 4.5%; Score 109; DB 4; Best Local Similarity 52.9%; Pred. No. 0.00096; Matches 18; Conservative 3; Mismatches 13

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Sequence 9, Application US/08810009
Patent No. 6211437
GENERA No. FORMATON:
APPLICANT: Briggs, Steven P.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 108; DB 4; Length 35;
Pred. No. 0.0012;
4; Mismatches 13; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
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COMPUTER: IBM PC compatible
OPERATUR: TSM PC COOPERATUR
SOFFWANE: Patentin Release #1.0, Version #1.30
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CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SPEUILL, W. MULTRAY
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5:
TELECOMMUNICATION INFORMATION
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                               APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
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50.0%;
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Best Local Similarity 50.09
Matches 17; Conservative
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TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                          GENERAL INFORMATION:
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281 ----NKEIG-DVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTT-EVWTYAIVE 333
                                           444 WGVHAGKDVGRGMAADIDPRYEGAEVWANGSLYTAKGV-KIGNTLPSSTNFGIW----- 496
                                                                                          334 KDMPEDLKRRLADSVQ-----RTVGPAGFWESDDNDNMETAS----QNG-KKYQSR 379
                                                                                                                     ----VYGDAVYPGVVGKSAIG--ETSY 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997 CLASSIFICATION: 800 CLASSIFICATION: 800 NAME: Spruill, W. MURTAY REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
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US-08-810-009-15
: Sequence 15, Application US/08810009
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TELECOMMUNICATION INFORMATION
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.99
Matches 18; Conservative
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; MOLECULE TYPE: protein
US-08-810-009-13
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| Patent No. 6211437
| GENERAL INPORMATION:
| APPLICANT: Briggs, Steven P. APPLICANT: Gray, John
| APPLICANT: Gray, John
| TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
| TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
| NUMBER OF SEQUENCES: 65
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: BELL, SELTZER, PARK & GIBSON
| STREET: P.O. Drawer 34009
| CITY: Charlotte
| CITY: Charlotte
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.4%; Score 106; DB 4; Length 35;
Best Local Similarity 51.4%; Pred. No. 0.0019;
Matches 18; Conservative 4; Mismatches 13; Indels
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APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997 CLASSIFICATION: 800
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04-MAR-1997
                                                                                                      REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-881-3145
TELEFAX: 919-881-3175
TELEFX: 575102
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MULTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELERX: 575102
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                         APPLICATION NUMBER: US/0
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-810-009-9
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                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-810-009-18
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ANT: IZUTESU, HITOSHI
ANT: IZUTESU, KAZUHLKO
NAT: MATSUMOCO, Akira
NAT: MATSUMOCO, Akira
NAT: MATSUMOCO, Akira
FINVENTION: CHLAMYDIA DIEUMONIAE ANTIGENIC POLYPEPTIDES,
FINVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
DE INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
FINVENTION: COMPAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
FINVENTION: ANTIBODY, METHOD AND REAGENTS FOR DIETECTION AND/OR MEASUREM
FINVENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
FINVENTION: MEASUREMENT OF CHLAMYDIA PROBUMONIAE GENE, AND PRIBMES FOR DETECTION AND
FINVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
FINVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
FINVENTION: CHLAMYDIAE GENE
CRECITED AND CHLAMYDIA
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                                                                                              Gaps
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    Score 104; DB 4; Length 35;
Pred. No. 0.0029;
2; Mismatches 14; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-MR 1997
CLASSIFICATION: 435
                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                               1 NSCRHRGALLCPFSKGNQKFHVCRYHGWSYDSSG 34
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATE: 28-APR-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 1000
FILING DATE: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 106006/95 FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 106008/95 FILING DATE: 28-APR-1995
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FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
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FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08809326A Patent No. 6165478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 869-8864/9741
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REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 74,
TELECOMMUNICATION INFORMATION:
4.3%; 4
milarity 52.9%; I
Conservative 2;
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INFORMATION FOR SEQ ID NO: 16:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                 Best Local Similarity
Matches 18; Conserv
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US-08-809-326A-16
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                 Query Match
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195 WKAPAENFVGDAYHVGWTHASSL-----RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 WNLPAD------LAWFKRNTLNKPVIMGRHTWESIGRPLPGR------KNIILSSQP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 649;
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21.4%; Pred. No. 0.28;
tive 38; Mismatches
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 7426-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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                                                                                                       PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INPORMATION:
  JP 106008/95
                                                                    JP 106009/95
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  NAME: Miller, Charles E. REGISTRATION NUMBER: 24,576
                  FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP IC
                                                                                      28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               649 amino acids
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Best Local Similarity 21.4%
Matches 53; Conservative
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MOLECULE TYPE: peptide
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                         FILING DATE:
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS, CARRYING THE DNAS, TRANSPORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD POR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DEFECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIFFIRMES FOR DEFECTION AND/OR MEASUREMENT
PREUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DEFECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                           171 -----DNQKNIMSQVLFSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAGASG 224
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                        195 WKAPAENFVGDAYHVGWTHASSL-----RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                119 VEGDTHFPDYEPDDWESVFSEFHDADAQNSHSYEFEILE-----RRILMSISSSSGP 170
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                                                                                                                                                                                                                                                                                                               247 GSGMGVLWDGYSGVHSADL-----VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
                                                                                                                                                                                                                                                                                                                                                                                                      V----FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGP 354
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                                                                                                                              Length 432;
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                                                                                                                              4.3%; Score 103.5; DB 4;
21.4%; Pred. No. 0.15;
tive 38; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/809,326A
FILING DATE: 19-MAR-1997
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APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08809326A Patent No. 6165478 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Obara, Kazuhiko
LENGTH: 432 amino acids TYPE: amino acid
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                                                          MOLECULE TYPE: peptide
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NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                 ; MOLECULE TYPE
US-08-809-326A-16
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US-08-809-326A-15
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                  TYPE: ami
TOPOLOGY:
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 27, 2003, 08:54:32; Search time 25.8333 Seconds (without alignments) 3581.232 Million cell updates/sec Run on:

US-09-843-250-2 2408 1 MNYNNKILVSESGLSQKHLI......AEFEHASSTWHTELTKTTDR 449 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 seqs, 206047115 residues Searched:

671580

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:* sp_bacteria:* SPTREMBL_21:* Database

sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_virus:* sp_vertebrate:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_fungi:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	Q938r9 pseudomonas	052142 pseudomonas			052382 ralstonia s	Q8vud4 burkholderi				O9etk2 pseudomonas		09f5t3 pseudomonas	Q9f5s8 pseudomonas	Q9f5s9 pseudomonas		
SOMMANTES			ΩI	Q938R9	052142	Q9ZI73	Q9L5D2	052382	Q8VUD4	P95564	Q8RTL4	045695	Q9ETK2	Q9F5S4	Q9F5T3	Q9F5S8	Q9F5S9	Q9F5S3	Q9EUC7
			DB	. 2	7	~	7	7	7	7	7	~	~	7	~	7	7	7	7
		Query	Length	449	449	449	447	447	447	447	447	451	277	277	277	277	277	277	277
	æ	Query	Match	96.8	95.1	91.7	91.0	6.06	86.2	85.3					61.7		61.6	60.3	58.3
			Score	2331	2291	2207	2192	2188	2075	2055	2026	1968.5	1490	1488	1486	1484	1483	1451	1405
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121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180

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			2 08VR24 2 08VR22 2 093NA8 2 09WR25 2 09WR25 2 09WR56	
277 277 277 275 772	772 772 772 772 772	277 277 277 226 214	214 214 214 214 208	206 214 303 297 297
	58.0 57.8 57.8 57.8 57.8	7.7.9.7.		
1403 1402 1399 1399	1396 1393 1393 1393	1390 1384 1354.5 1139	1127 1123 1112.5 1067 1044.5	1039 1038 1038 1016 1009
17 18 19 20 21	22 22 24 26 27	28 30 32 33	, w w w w w w 4 rv o v o o	044444 0110040

ALIGNMENTS

RESULT 1 0938R9 AC 0938R9; DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) DE Naphthalene dioxygenase. DE Naphthalene dioxygenase. CN Napedomonas fluorescens. CN Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; CN Pseudomonas. CN NOBI_TAXID=294; RN [1] RN NOBI_TAXID=294; RN [1] RN SEQUENCE FROM N.A. RA Min KH. Ji SH.; RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. RM Min KH. Ji SH.; RN SEQUENCE FROM N.A. RA Min RH. Ji SH.; RN SEQUENCE FROM N.A. RA Min RH. Ji SH.; RN SEQUENCE FROM N.A. RA SEQUENCE RAPOSO STATE SERVER. DR Pfam: PPC09888 Ring—hydroxyl_A. 1. DR Pfam: PPC09888 Ring—hydroxyl_A. 1. DR Pfam: PPC08488 Ring—hydroxyl_A. 1. DR PKOSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1. NW Dioxygenase. SQ SEQUENCE 449 AA: 49608 MW; SEFEDBE0282FE812 CRC64; AQUery Match Best Local Similarity 96.0%; Pred. No. 3.9e-171; Matches 431; Conservative 12; Mismatches 6; Indels 0; Gaps OV HINTUNINSESCLEGARHLINGDEBLEOHERFTTERARMLETHPELIPPELIPPEDIP	Db 1 MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIFARNWLFLTHDSLIPSPGDYVTAKMG 60
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Matches 424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAKIZAWA N., Kaida N., Torigoe S., Moritani T., Sawada T., Satoh S.
                                        QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                            FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                                        FPNNSVLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADAVQRTFGPAGFWES
                                                                                                                                                    DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                              ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosomes of Pseudomonas aeruginosa PaK1 and Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noboru T., Toshiya I., Takashi S., Kazuhiro Y., Masamichi K.
Yue-Wu W., Masao F., Hohzoh K.;
"The molecular analysis of NAH7-type cluster located on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00355, Rieske; 1. Pfam; PF00355, Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
CFOHENCE 449 AA; 49361 MW; 80020F54AAB11E8A CRC64;
                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Iron-sulfer protein large subunit.
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Pred. No. 4.7e-168;
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HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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MEDLINE-94209249; PubMed-8157615;
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Best Local Similarity
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SEQUENCE FROM N.A.
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Q52142; O08194;
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                                                                                                                                                                                                                                                                                                                                                                                                            Takizawa N.;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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Last annotation update)
12;
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  Mismatches
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01-MAY-1999 (TrEMBLrel. 10, Last sequence u
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Naphthalene dioxygenase Fe-S large subunit.
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF008489; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDTOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
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13;
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Gene 286:149-157(1999).
EMBL: AR039533; AAD02136.1; 'HSSP; P23094; 1NDO.
Conservative
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                                               119 KELYGDAIKKKCLGLKEVPRIESFHGFIYGCFDAEAPPLIDYLGDAAWYLEPIFKHSGGL
                                                                                                            KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
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"nag genes of ralstonia (Formerly pseudomonas) sp. Strain U2
enzymes for gentisate catabolism.";
Ensteriol. 183:700-708(2001).
EMBL: AF036940; AAD12610.1; -.
HSSP; P23094; 1NDO.
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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Last annotation update)
large oxygenase component.
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89.1%; Pred. No. 3.9e-160;
ive 25; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; I.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGRNSE.
PROSITE; PS00570; RING_HYDROXXL_ALPHA; 1.
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SEQUENCE 447 AA; 4
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"Insights into the genetic diversity of initial dioxygenases from PAH-degrateria."
Appl. Microbiol. Biotechnol. 55:609-618(2001).
EMBL; AF252550; AAF72976.1; -.
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                                                               KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
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llarity 88.9%; Pred. No. 1.9e-160;
Conservative 27; Mismatches 21;
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InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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MEDLINE=21306905; PubMed=11414329;
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Best Local Similarity
Matches 399; Conserv
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SEQUENCE
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RESULT 6

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121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                        119 KELYGDAIKKKCLGIKEVPRIESFHGFIYGCFDAEAPPLIDYLGDAMYLEPTFKHSGGL 178
                                                                                                                                                                                         181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
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 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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"Cloning and sequencing of the genes encoding 2-nitrotoluene dioxygenase from Pseudomonas sp. JS42.";
Gene 181:57-61(1996).
EMBL: U49504; AAB40383.1; -
HSSP; P23094; INDO.
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Pfam; PF00155; Rieske; 1.
Pfam; PF00155; Rieske; 1.
Pfam; PF001848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSTIE; PS0050; RNGDIOXGNASE.
SEQUENCE 447 AA: 49465 MW; ICB0E223E528E3BD CRC64;
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Last annotation update)
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83.7%; Pred. No. 6.7e-150;
iive 35; Mismatches 36;
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InterPro; IPR001663; Ring_hydroxyl_A
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MEDLINE=97128768; PubMed=8973308;
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Best Local Similarity 83.7
Matches 376; Conservative
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NCBI_TaxID=306;
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01-MAY-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                                                                                                                                        QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKE1GDVRARIYRSHLNCTV
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                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson G.R., Jain R.K., Spain J.C.; "Properties of the trihydroxytoluene oxygenase from Burkholderia cepacia R34: an extradiol dioxygenase from the 2,4-dinitrotoluene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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Johnson G.R., Jain R.K., Spain J.C.;
Johnson G.R., Jain R.K., Spain J.C.;
Johnson G. the 2,4-dinitrocluene pathway.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF169302; AAL50021.1;
InterPro; IPR001281; Rieske.
InterPro; IPR00163; Ring_hydroxyl_A.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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49468 MW; 2A5BF8558320275C
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Pfam; PF00355; Ricske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRNUNS; PR00090; RWGDIOXXGNASE.
PROSTTE; PS00570; RING_HYDROXXL_ALP
SEQUENCE 447 AA; 49468 MW: 2AFN
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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"Molecular Characterization and Substrate Specificity of Nitrobenzene Dioxygenese from Comamonas sp. Strain JS765.";
Appl. Environ. Microbiol. 68:534-641(2002).
EMBL; AF379638; AAL76202.1;
SEQUENCE 447 AA; 49556 MW; 4CA961F99A37DF3A CRC64;
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Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas
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larity 82.0%; Pred. No. 1.1e-147;
Conservative 41; Mismatches 38;
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MEDLINE=21681044; PubMed=11823201;
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Best Local Simi
Matches 368;
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Bacteria; Proteobacteria; beta subdivision; Burkholderia
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Pfam; PF00185; Rieske; 1.
PF10175; PF001809; RNGD10XGNAS.
PROSTITE; PS00150; RNGD10XGNAS.
SEQUENCE 451 AA; 49827 MW; 726796C29CEF9A10 CRC64;
                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.7%; Score 1968.5; DB 2;
80.0%; Pred. No. 3.1e-143;
ive 41; Mismatches 46; :
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                                                                                                                                                                                                                                                                                                 451
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"2,4-Dinitrotoluene dioxygenase from Burk
similarity to naphthalene dioxygenase.";
" Bacteriol. 178:4926-4934(1996).
EMBL; U62430; AAB09766.1; -.
HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                             QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DNT;
MEDLINE=96326338; Pubmed=8759857;
                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
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423

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Q9ETK2

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121 HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAAIPP 180
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                                                                                                                                                                                              Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase genes (nahAc)
Pseudomonas strains from West Mediterranean Sea.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AF306440; AAG25700.1;
HSSP; P30944, INDD.
InterPro; IPR001281; Rieske.
InterPro; IPR001281; Ring_hydroxyl_A.
Pfam; PF000355; Riseske: 1.
Pfam; PF00048; Ring_hydroxyl_A; I.
PR00090; RNGDIOXGNASE.
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Coexistence of two naphthalene dioxygenase genes (nahAc)
Pseudomonas strains from West Mediterranean Sea ";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FADFDA5D37E241AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%; Score 1488; DB 2;
99.6%; Pred. No. 1.4e-106;
live 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30094 MW;
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Matches 276; Conservative
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277 AA;
                                                                        Pseudomonas putida
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                                                                                                                                                                                   STRAIN-SIIIASAL;
                                                                                                                             NCBI_TaxID=303;
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NON_TER
NON_TER
SEQUENCE 27
                                                                                                              Pseudomonas.
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Q9F5T3
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Pseudomonas
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Perrero M.A., Lalucat J., Bosch R.;

Coexistence of two maphthalmed dioxygenase genes (nahAc) in Ferrero M.A.; Lalucat J., Bosch R.;

Coexistence of two maphthalmed dioxygenase genes (nahAc) in Pseudomonas strains from West Mediterranean Sea.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR306438; AAG25698.1; -.

EMBL; AR306436; AAG25698.1; -.

EMBL; AR306436; AAG25698.1; -.

EMBL; AR306431; AR306438; RAG25698.1; -.

INTERPRO; IPRO01281; Rieske.

InterPro; IPRO01281; Rieske.
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                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein 2. (Fragment)
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                                                      421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                            Q9F5S4;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                 PRT;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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30094 MW;
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Matches 277; Conservative
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61 SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGGFDQEAPPLMDYLGDAWYLEPMFK 120
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                                                                                                  116 SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                                                                                                                                               EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH 295
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                                                  1 TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrero M.A., Lalucat J., Bosch R.;

"Coexistence of two naphthalene dioxygenase genes (nahac) in Pseudomonas strains from West Mediterranean Sea.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF306433; AAG25693.1;

Therpro: IPR00181; Rieske.

InterPro: IPR00181; Rieske.

InterPro: IPR001863; Ring_hydroxyl_A.

Pfam; PF00345; Rieske: 1.

Pfam; PF00848; Ring_hydroxyl_A: 1.

Pfam; PR009095; Ring_hydroxyl_A: 1.

Pfam; PR0090950; Ring_hydroxyl_A: 1.
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      1; Indels
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16, Last sequence update)
19, Last annotation update)
iron sulfur protein (Fragment)
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     0; Mismatches
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     Matches 276; Conservative
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Matches 276; Conserv
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01-MAR-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                         SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                                                                                                                                                                                                                                                                        HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
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                                                                                                                                                                                                               Length 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase genes (nahAc) :
"Seudomonas strains from West Mediterranean Sea.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR306434; AAG25694.1; -.
HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR011281; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein (Fragment).
                                                                                                                                            1 1
277 277
277 AA; 30064 MW; DB47868EB6DD525A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30064 MW; 6BFF83D32F04CFC3 CRC64;
                                                                                                                                                                                                         61.7%; Score 1486; DB 2;
99.6%; Pred. No. 2.1e-106;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1484; DB 2;
Pred. No. 2.9e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 332
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                            InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIGOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
EMBL; AF306426; AAG25686.1; -. HSSP; P23094; 1NDO.
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99.6%;
                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AA;
                                                                                                                                                                                                                           Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=139773;
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                                                                                                                              Dioxygenase.
NON_TER
NON_TER
SEQUENCE 27
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NON_TER
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SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                            Query Match
Best Local (
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Gaps

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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.3%; Score 1451; DB 2; Length 277; Best Local Similarity 96.8%; Pred. No. 1e-103; Matches 268; Conservative 6; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein 1 (Fragment)
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277 277
277 AA; 30062 MW; 82C78D865A92D0AB CRC64;
                                                                                        296 LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 332
                                                                                                                       241 LNCTVFPNNSVLTCSGVFKVWNPIDANTTEVWTYAIV 277
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Pfam; PF004848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RING_HYDROXYL_ALPHA; 1.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
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                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=303;
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SEQUENCE 27
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 27, 2003, 08:47:32; Search time 7.16667 Seconds (without alignments) 2598.540 Million cell updates/sec Run on:

US-09-843-250-2 2408 1 MNYNNKILVSESGLSOKHLI......AEFEHASSTWHTELTKTTDR 449 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

	Q9y3f4 homo sapien			Q9bzf1 homo sapien				P28868 candida alb			P51851 pisum sativ		
	UNRI_HUMAN	F26_YEAST	ATPA_ENTHR	ORP8_HUMAN	SYI_STAAU	DHE3_PYRKO	POLN_HEVMY	GBA1_CANAL	DLG3_MOUSE	DLG3_RAT	DCP2_PEA	AGLU_ASPOR	
	П	П	Н	П	Н	Н	Н	~4	П	Н	٦	Н	
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\	χ. υ.	94.5	94.5	94	94	93	93	92.5	92.5	92.5	92	92	
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                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
SPECIES-P.putida; STRAIN-NCTB 9816;
MEDLINE-98298434; PubMed-9634695;
Rauppi B., Lee K., Carredano E., Parales R.E., Gibson D.T., Eklund H., Ramaswamy S.;
                                                                                                                    O.F
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00355; Rieske; I. Pfam; PF00355; Rieske; I. Pfam; PF00848; Ring_hydroxyl_A; 1. PRINTS; PR00099; RNGDIOXGNASZ. PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1. Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron; Dioxygenase; NAD; Plasmid; 3D-structure.
                                                                                   Structure of an aromatic-ring-hydroxylating dioxygenase-naphthalene
                                                                                          N -> K (IN STRAIN G7).
S -> F (IN STRAIN ATCC 17484).
S -> T (IN STRAIN G7).
S -> R (IN STRAIN G7).
A -> S (IN STRAIN G7).
N -> S (IN STRAIN G7).
                         Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> NA (IN STRAIN G7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON-SULFUR (2FE-2S).
IRON-SULFUR (2FE-2S).
IRON-SULFUR (2FE-2S).
IRON-SULFUR (2FE-2S).
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PIR: B49343; B49343.

PDB; INDO: J23-MAR-99.

InterPro: IPR001281; Rieske.
SEQUENCE FROM N.A.
SPECIES-P.putida; STRAIN-ATCC 17484;
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15-JUN-2002 (Rel. 41, Last annotation update)
Naphthalene 1,2-dioxygenase alpha subunit (EC 1.14.12.12) (Naphthalene
1,2-dioxygenase ISP alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                   61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                   121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                             1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
                                                                                                                                                                                                                                                                           1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
- MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION (BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CISNAPHTHALENE DIHYDRODIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) - (1R,2S)-1,2-
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E (IN STRAIN G7).

I (IN STRAIN G7).

A (IN STRAIN G7).

C (IN STRAIN G7).

V (IN STRAIN G7).

V (IN STRAIN G7).

K (IN STRAIN G7).

K (IN STRAIN G7).
                                                                                                                                                                                                       Length 449;
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 D -> E (IN STRAIN G7).
S -> A (IN STRAIN G7).
S -> C (IN STRAIN G7).
S -> C (IN STRAIN G7).
A -> V (IN STRAIN G7).
E -> K (IN STRAIN G7).
C -> K (IN STRAIN G7).
H -> D (IN STRAIN G7).
H -> D (IN STRAIN G7).
                                                                                                                                                                                                  Score 2403; DB 1;
Pred. No. 2.6e-181;
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                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDOB_PSEFL STANDARD; F 007824; 15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                  49607 MW;
                                                                                                                                                                                                      99.8%;
99.8%;
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449 AA;
                                                                                                                                                                                                                      Similarity
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NDOB_PSEFL
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in ow we modified and this statement is not removed. Usage by and for commercia
dihydronaphthalene-1,2-diol + NAD(+).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

PATHWAX: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES
CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF
DIBENACTHIOPHENE (DBT) AND PHENNATHRENE. CONVERTS PHENANTHENE TO
1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DBT IS LIMITED TO
OXIDATION OF THE AROMATIC RING.
                                                                          SUBGNITT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT AND AN IRON SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN REDUCTAGE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS COMPOSED OF A LARGE ALPHA SUBGNIT (NDOB) AND A SMALL BETA SUBGNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                     InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00048; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSTITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Dioxygenase; NAD; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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Pred. No. 1.
                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                        DIOXYGENASE ALPHA SUBUNIT FAMILY.
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95.5%;
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449 AA;
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Best Local Similarity
Matches 429; Conserv
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                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Naphthalene 1,2-dioxygenase alpha subunit (EC 1.14.12.12) (Naphthalene
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361 DDNDNMETASQNGKKYQSRDSDLISNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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PROSTTE; PSO0570; RING_HYDROXYL_ALPHA; 1. Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1,2-dinydronaphthalene-1,2-diol + NAD(+).

GOFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES
CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF
DIBENZOTHIOPHENE (DBT) AND PHENAMTHRENE. CONVERTS PHENANTHRENE
1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DBT IS LIMITED
OXIDATION OF THE AROMATIC RING.
SUBUNIT: NAPHTHALENE DIOXXCENASE (NDO) MULTICOMPONENT ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The molecular analysis of an NAH7-type gene cluster, pah, located the chromosome of Pseudomonas aeruginosa PaK1."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF NAHALENE DIOXYGENASE (NDD) MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION BOTH ATOMS OF WOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CIS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
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                                                      421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                  InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
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                                                                                                                            KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                               9
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                                                           Gaps
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040139; P7590; P78203;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
3-phenylpropionate dioxygenase alpha subunit (EC 1.14.1.-)
(Digoxigenin alpha subunit).
HCAE OR PHDCI OR HCAA OR HCAAI OR DIGA OR B2538 OR Z3809 OR ECS3404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                       1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                121 KELYGBALDKKCMGLKEVARVESFHGFIYGCFDEBAPSLKDYMGDAGWYLEPMFKHSGGL
                                                                                                                                                                                                       241 OMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGEVRARIYRSHLNCTV
                                                                                                                                                                                             ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                   QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKE1GDVRAR1YRSHLNCTV
                                                                                                                                                                                                                                                                        FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
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                                                          23; Indels
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Turlin E., Gasser F., Biville F.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                       Length
 213 IRON (BY SIMILARITY).
362 IRON (BY SIMILARITY).
49715 MW; 35A189136722A21C CRC64;
                                     Score 2218; DB 1;
Pred. No. 8.8e-167;
                                                         23; Mismatches
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                                       92.18;
                                              89.88;
                                                         Matches 403; Conservative
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213 2
362 3
449 AA;
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STRAIN-K12 / MG1655;
                                                Local Similarity
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CSTRAIN-015:H7 (RIMD 0508952;

XX BDLINE-21156231; PubMed-11258796;

XA Hayashi T., Makino K., Ohhishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohhishi M., Rurokawa C., Osasawara M., Tobe T.,

XA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

XA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

XA Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

XA Complete genome sequence of enterohemorrhagic Escherichia coli

"Complete genome sequence of enterohemorrhagic Escherichia coli

TO157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

CONVERTS 3-PHENYLPROPIONIC ACID (PP. INTO CIS-3-(3-CARBOXYETHYL)-3-5-CYCLOHEXADIENE-1,2-DIOL (PP-DIHYDRODIOL).

S. SCYCLOHEXADIENE-1,2-DIOL (PP-DIHYDRODIOL).

S. SCYCLOHEXADIENE-1,2-DIOL (PP-DIHYDRODIOL).

S. SCYCLOHEXADIENE-1,2-DIOL (PP-DIHYDRODIOL).

S. SCYCLOHEXADIENE-1,2-DIOL (PP-DIHYDRODIOL).

S. SCHWAY: 3-Phenylpropionic acid catabolism.

C. I- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: THE TWO SUBUNITS OF THE HYDROXYLARD (MCAC) AND A FERREDOXIN REDUCTASE (HCAD).

C. I- SUBUNITS: BELONGS TO THE BACTERIAL RING-HYDROXYLATING

DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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InterPro: IPR001281; Rieske.
InterPro: IPR001683; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; l.
Pfam; PF00355; Rieske; l.
Pfam; PF00948; Ring_hydroxyl_A; l.
PRINTS; PR00090; RING_HYDROXYL_APHA; l.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                      Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampel G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horluchi T.; Takeda J., Takemoto K., Uehara K., Wada C., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Tagami B., Horluchi T.; Takeda J., Takemoto K., Uehara K., Wada C., Tagami B., Horluchi T.; Takeda J., Takemoto F., Uehara K., Wada C., Tagami B., Horluchi T.; Takeda J., Takemoto F., Uehara K., Wada C., Tagami B., Horluchi T.; Takeda J., Takemoto F., Uehara K., Wada C., Tagami B., Horluchi T.; Takeda J., Takemoto F., Uehara K., Wada C., Tagami B., Horluchi T.; Takeda J., Takemoto F., Uehara K., Wada C., Tagamata S., Horiuchi T., Takemoto F., Takemoto F., Uehara K., Wada C., Takemoto F., Uehara K., Wada C., Tagamata S., Horiuchi T., Takemoto F., Wamata S., Horiuchi T., Takemoto F., Wamata S., Wamata S., Horiuchi T., Takemoto F., Wamata S., Wamata S., Horiuchi T., Takemoto F., Wamata S., W
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SIMILARITY).
SIMILARITY).
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MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Welchen Sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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MEDLINE-97349980; PubMed-9205837;
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EMBL; D90883; BAA16433.1; -.
EMBL; D90884; BAA16441.1; -.
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                                     V -> A (IN REF. 1).
GHRARNSKLCLEMGLGQEKRRDDGIPGITNYIFSETAARGM
                                                              YQRWADLLSSESWQEVLDKTAAYQQEVMK -> ATAPATAN
CVWKWGLVRKSAATTAFLALLTISFQKLPLVECTNAGPIF
                                                                                                                                                                                                                            VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                                                 84 OCRHRAMRVSYADCGNTRAFTCPYHGWSYGINGELIDVPLEPRAYPOGLCKSHWGLNEVP 143
                                                                                                                                                                                                                                                                                                                                            RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP 198
                                                                                                                                                                                                                                                                                                                                                                                                      QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE------AEQRLGEVRALRL 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS 412
                                                                                                                                                                           20 IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                          |: | :::| ||: || || ||| ||:| || |||:
24 IYTDPDIYQLEEERIFGRCWLFLAHESQIPKPGDFFNTYMGEDAVVVVRQKDGSIKAFLN
                                                                                                                                                                                                                                                                                         IRON-SULFUR (2FE-2S) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                             199 AENFVGDAYHVGWTHASSL------RSGESIFSSLAGNAALP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tan H.-M., Tang H.-Y., Joannou C., Abdel-Wahab N.H., Mason J.R., "The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenase are unusual in codon usage and low in G+C content.", Gene 130:33-39(1993).
                                                                                                                                                     50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-dihydrobenzene-1,2-diol + NAD(+).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
PATHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.
                                                                                                                           Length 453;
                                                                                                                                                    Indels
                                                                                                   02535BF5F47643FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Benzene 1,2-dloxygenase alpha subunit (EC 1.14.12.3).
             (BY SIMILARITY).
                                                                                                                        ^ Match 30.6%; Score 736; DB 1; L. Local Similarity 36.4%; Pred. No. 2.3e-50; les 165; Conservative 64; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
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                                                                                       (IN REF.
             IRON
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01-NOV-1995 (Rel. 32, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                   MW.
                                                                                                   51109
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108
213
218
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453
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Plasmid pHMT112.
                                                                                                   453 AA;
108
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384
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Q07944;
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                      METAL
CONFLICT
CONFLICT
                                                                                                  SEQUENCE
                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
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SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ
                        (BEDC1 AND BEDC2),
SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BEDC1 AND BEDC2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 450;
                                      FERREDOXIN (BEDB) AND A FERREDOXIN REDUCTASE (BEDA). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
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IRON-SULFUR (2FE-2S)
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IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNDIOXGNASE.
PROSTITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 651.5; DB 1; Pred. No. 9.8e-44; 69; Mismatches 174
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                                                            SIMILARITY: BELONGS TO THE BACTER DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001281; Rieske.
Interpro; IPR001663; Ring_hydroxyl_A.
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119
122
1RC
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1RC
51108 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dioxygenase; NAD; Plasmid.
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98
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450 AA;
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es 148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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TOD1_PSEPU
ID TOD1_PS
AC P13450;
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PIR; B41858; B41858.
                                                                                                                      443
                                                                                                   428 NW 429
                                                                                                                                                                  BPHA_BURCE
P37333;
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                                                                                                                                                         BPHA_BURCE
                                                                                                                      442
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                                                                                                                                                  RESULT 7
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                                                                                                                                                                     the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 VLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML 307
                                                                                                                         PRINTS; PR00090; RNGDIOXGNĀSĒ.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
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SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                      Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181; Indels
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01.JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Toluene 2,3-dioxygenase alpha subunit (EC 1.14.12.-).
                                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON (BY SIMILARITY)).
                                                                                                                     Zylstra G.J., Gibson D.T.;
"Toluene degradation by Pseudomonas putida Fl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 649.5;
                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
8
                                                                                                                                                                                                                                                                                                                                           Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                PIR; A36516; A36516.

HSSP; P23094; INDO.
InterPro; IPRO01281; Rieske.
InterPro; IPRO01663; Ring_hydroxyl_
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                            PubMed=2670929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50944 MW;
                                                                                                                                                                                                                                                                                                       EMBL; J04996; AAA26005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.0%;
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98
1116
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228
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                                               Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                            MEDLINE-89359301;
                                                                                                                                                                                                                                                                                                                                                                                                  Dioxygenase; NAD
                                                                        NCBI_TaxID=303;
                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 145;
                                                                                                   STRAIN-F1;
                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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264 GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAPERLGSVERGSKLMVEHM--TVFPTCSFL 321
                                                                                                               TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWESDDNDNME 367
                                                                                                                                                             322 PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRROTLRTFSAGGVFEODDGENWY 381
                                                                                                                                                                                                                                                                 368 TASONGKKYOSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS 427
                                                                                                                                                                                                                                                                                                            382 EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haddock J.D., Gibson D.T.;
J. Bacteriol. 178:2158-2158(1996).
-!- CATALYITC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit.
-!- PATHWAY: Biphenyl-polychlorinated biphenyl degradation pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BphE subunits. A ferredoxin (BphF) and a ferredoxin reductase (BphG) must be present to obtain activity. SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biphenyl dioxygenase alpha subunit (EC 1.14.12.18) (Biphenyl 2,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rerization of the oxygenase component of from Pseudomonas sp. strain LB400.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequencing and transcriptional mapping of the genes encoding biphenyl dioxygenase, a multicomponent polychlorinated-biphenyl-degrading enzyme in Pseudomonas strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     first step.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-10, AND CHARACTERIZATION.
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"Purification and characterization of
biphenyl 2,3-dioxygenase from Pseudomo
J. Bacterlol. 177:5834-5839(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 174:2903-2912(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92234948; Pubmed=1569021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
15-JUN-2002 (Rel. 41, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erickson B.D., Mondello F.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burkholderia.
NCBI_TaxID=292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dioxygenase).
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                                                                                                                                                                                                                                          DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                           SVQRTVGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKS 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comamonas
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                     131 KCLGLKEV-----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELV
                                                                                                                                                                                                                                                                                         GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL
                                                                                                                                                                                                                                                                                                                               QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAK-------QERLNKEIGD
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                                                                                                                                                                                                                                                                                                                                                                                            VRARIYRSHINCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                                                                                                                                                                              VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR
                                                                                                                                                                                     43;
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                                                                                                                                                                    Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12.18) (Biphenyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97045812; PubMed-8890734; Sirois M., Hurtubise Y., Bergeron J., Ahmad
                                                                                                                                                                                     Indels
                                                                                         IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                                                                                                   DB 1;
                                                                                                                                                                                    Mismatches 186;
                                                                                                                                                                 Score 616.5; DB 1
Pred. No. 5.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
                         Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDLOXGANSE.
PROSITE; P800570; RING_HYDROXYL_ALPHA;
Aromatic hydrocarbons catabolism; Oxido
                 Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 AIGETSYRGFYRAYQAHVSSSNWA 430
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                                                                                                                                                                                    :69
                                                                                                                                                51382 MW;
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        InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hy
                                                                                                                                                                  25.6%;
32.9%;
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101
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458 AA;
HSSP; P23094; 1NDO
                                                                                                                                                                           Similarity
                                                                       Dioxygenase; NAD.
INIT_MET 0
METAL 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dioxygenase).
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Matches 146;
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Q46372;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             SUBUNIT: Heterohexamer consisting of three BphA subunits and three BphE subunits. A ferredoxin (BphF) and a ferredoxin reductase (BphG) must be present to obtain activity (By similarity). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
Shareck F., Barriault D., Guillemette I., Juteau J.M.; "Sequencing of Comamonas testcosteroni strain B-356—biphenyl/chlorobiphenyl dloxygenase genes: evolutionary relationships among Gram-negative bacterial biphenyl dioxygenases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIK 192
                                                                                                           Gene 174:195-202(1996).
-!- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-phenyl.cyclohexa 3,5-disne-1,2-diol + NAD(+).
-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit (By
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Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
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D133FC0635FACBF5 CRC64;
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6.1e-41;
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InterPro; IPR001663; Ring_hydroxyl_A.
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Pfam; PF00848; Ring_hydroxyl_A;
PRINTS; PR00090; RNGDIOXGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBUNIT: Heterohexamer consisting of three BphA subunits and three BphE subunits. A ferredoxin (BphE) and a ferredoxin reductase (BphG) must be present to obtain activity (By similarity).
-: SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
381 VFEODDGENWVEIORVMRGHKAKSTSLCAKMGLNVPNKNNPAYP---GKTAYVYAEEAAR 437
                                                                                                                                                                                                                                                                                                                                                                                   Taira K., Hirose J., Hayashida S., Furukawa K.;
"Analysis of bph operon from the polychlorinated biphenyl-degrading strain of Pseudomonas pseudoalcaligenes KF707.";
J. Biol. Chem. 267:4844-4853(1992)
-:- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-:- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF00355; Rieske; ...; Pfam: PF00355; Rieske; ...; Pfam: PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                Pseudomonas pseudoalcaligenes.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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33.1%; Pred. No. 6.1e-41;
.ive 70; Mismatches 183; Indels
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Interpro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                         STRAIN=KF707;
MEDLINE=92165849; PubMed=1537863;
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Matches 147; Conservative
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GMYHHWSRMMSEPSW 452
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BPHA OR BPHA1
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                           DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
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                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Benzene 1,2-dioxygenase alpha subunit (EC 1.14.12.3) (P1 subunit).
                                                                                               KCLGLKEV-----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELV
                                                                                                                                                                                                                                                                                             QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAK-------QERLNKEIGD
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                                                                                                                                                                                              GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL
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"Nucleotide sequencing and characterization of the genes encodin benzene oxidation enzymes of Pseudomonas putida.";
J. Bacteriol. 169:574-5179(1987).
-!- CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-diptrobenzene-1,2-diol + NAD(+).
-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-!- PATHWAY: FIRST STEP OF DECRADATION OF BENZENE TO CATECHOL.
-!- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS:
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HSSP; P23094; 1NDO.
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SYRGFYRAYQAHVSSSNW 429
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                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                         PGINTVRTLASARAERGEVWAFTVVDADAPDDIKEEFRARLRTFSPVACSSRTTGRTG-- 379
                                                                                                                                                                                                                                                                                                                                                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                              strains
                                                                                                                                                                                                                                    VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                                                                           --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                             Gaps
                                                                                                                                                                                             20 IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                          PRINTS; PR00090; RNGTIOXGRASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                     SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                      VLWDGYSGVHSADLVPELMAF - - GGAKQERLNKEIGDVR - - ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                                                                                                                                                                     264 GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
                                                                                                                                                                                                                                                                                                                                                                                             TCSGVFKVWNPIDANTIEVWTYAIVEKDMPEDLKRRLADSVQ------RTVGPAGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                  ESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYR
                                                                                                                                                                                                                                                       QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                                                                                                                                                                                                              WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12.18) (Biphenyl 2,3-
                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94324977; PubMed=8048958; Fukuda M., Yasukouchi Y., Kikuchi Y., Nagata Y., Kimbara K., Fukuda M., Yasukouchi Y., Tanagi M., Yano K.; Indentification of the bphA and bphB genes of Pseudomonas sp. skKS102 involved in degradation of biphenyl and polychlorinated
                                                                                                                                                     Score 588.5; DB 1; Length 448;
Pred. No. 8.6e-39;
8; Mismatches 176; Indels 45
                                                                          IRON-SULFUR (2FE-2S) (BY SII IRON-SULFUR (2FE-2S) (BY SII IRON-SULFUR (2FE-2S) (BY SII IRON-SULFUR (2FE-2S) (BY SII IRON (BY SIMILARITY).

IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
         IPR001663; Ring_hydroxyl_A.
                   Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp. (strain KKS102).
                                                                                                                                                                           68;
                                                                                                                                     50208 MW;
                                                                                                                                                      32.98;
 InterPro; IPR001281; Rieske
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                           96
98
116
119
222
228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 AYQAHVSSSNW 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HWLRMMTSPDW 441
                                                                                    98
116
119
222
228
448 AA;
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=307;
                                                                  Dioxygenase;
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dioxygenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BPA1_PSES1
Q52438;
                                                                                                                                                                           Matches 142;
           InterPro
                                                                                                                                    SEQUENCE
                                                                                                                                                       Query Match
                                                                                                                                                                   Best Local
                                                                                              METAL
METAL
                                                                                                                  METAL
                                                                                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQFRAAWGGHGSGWFINDAAILMAVMGPKITQYWTQGPAAEKAAKRLNQMPTQTMFGQHM 323
Biochem. Biophys. Res. Commun. 202:850-856(1994).
-!- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-phenylcyclohexa-3,5-diane-1,2-diol + NADH+).
-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit (By
                                                                                                                                                                           BphA2 subunits. A ferredoxin (BphA3) and a ferredoxin reductase (BphA4) must be present to obtain activity (By similarity). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                PATHWAY: Biphenyl-polychlorinated biphenyl degradation pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TVFPTCSFLPGINTIRSWHPRGPNEVECGPSWSSMPMR---PEDIKEEFRRONIRTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 IYADQDLYEIELERIFARSWLLLGHEAHIPKTGDYLTTYMGEDPVIMVROKDGSIKVFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEGAGLQMT----SKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGMGVLWDGYSGVHSADLVPELMAFGGAK------QERLNKEIGDVRAR-IYRSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCTVFPNNSMLTCSGVFKVWNPIDANTTEV---WTYAIVEKDMPEDLKRRLADSVQRTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA - - IGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e-38;
65; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
(BY
(BY
(BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON SYLFUR (2FE-2S) (IRON (BY SIMILARITY))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51876 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.3%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D17319; BAA04137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 33.6
es 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
103
121
124
234
240
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103
121
124
234
240
458 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dioxygenase; NAD.
                                                                                                          similarity)
                                                                                                                                                     first step.
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us-09-843-250-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - FUNCTION: DEGRADATION OF BENZOATE TO 2-HYDRO-1, 2-DIHYDROXYBENZOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequences of the Acinetobacter calcoaceticus benABC genes
 139 ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00355; Rieske; 1.
Pfam: PF00355; Rieske; 1.
Pfam: PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RING_DIXPROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for benzoate 1,2-dioxygenase reveal evolutionary relationships among multicomponent oxygenases.";
J. Bacteriol. 173:5385-5395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- PATHWAY: DEGRADATION PATHWAY LEADING FROM BENZOATE TO CATECHOL.
-i- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEINS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BENA AND BENB), AND AN ELECTRON TRANSFER COMPONENT (BENC).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                         GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPNNSML
                                  ARFASYRGFLFGSLREDVAPLEEFLGESRKVIDMVVDQSPEGLEVLRGSSTYVYEGNWKV
                                                                     198 PAENFVGDAYHVG---WTHASS-----LR-SGESIFSSLAGNAALPPEGAGLQMTSKYGS
                                                                                         26 GHQMVWARWGDPKNRPLF-----AERDRLASEFGEARADWMIGVSRNLCLYPNLYLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Benzoate + NADH + O(2) - catechol + CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD(+).
-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neidle E.L., Hartnett C., Ornston N.L., Bairoch A., Rekik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elby D.M., Neidle E.L.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10).
                                                                                                                                                                                                             308 TCSG-VFKVWNPIDANTTEVWTYAIVEK-DMPEDLKR 342
                                                                                                                                                                                                                                     | : |: || | | : | | : | 318 DQFGSQLRITRPLSVDRTEITIYCIAPKGETPRRARR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 84; 103-104; 171-172 AND 380-382
                                                                                                                                                                                                                                                                                                                                       461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S23477; S23477.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BD413 / ADP1;
MEDLINE=91358314; Pubmed=1885518;
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF009224; AAC46436.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter calcoaceticus.
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harayama S.;
                                                                                                                                                                                                                                                                                                                                       BENA_ACICA
                                                                                                                                                                                                                                                                                                                     BENA_ACICA
                                  152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             gene
members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (XYLX AND XYLY), AND AN ELECTRON TRANSFER COMPONENT (XYLZ).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lur. J. Blochem. 204:113-120(11992).
-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-!- PATHWAY: DEGRADATION OF BENZOATE AND TOLUATE TO CATECHOL.
-!- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEINS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                        "Cis-diol dehydrogenases encoded by the TOL pWWO plasmid xylL and the Acinetobacter calcoaceticus chromosomal benD gene are of the short-chain alcohol dehydrogenase superfamily.";
                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92155191; PubMed-1740120;
Neidle E.L., Hartnett C., Ornston L.N., Bairoch A., Rekik M.,
Harayama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 410.5; DB 1; Length 4; Pred. No. 8.4e-25; 64; Mismatches 135; Indels
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                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
1-NOV-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Toluate 1,2-dioxygenase alpha subunit (EC 1.14.12.-).
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                                                                                                        454 AA
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InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                        PRT;
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31.2%;
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Best Local Similarity 31.2 Matches 105; Conservative
                                                                                                        STANDARD;
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115
221
226
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                   NCBI_TaxID=303;
                                                                                                                                                                                                                                                Plasmid TOL
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                                                                                                    XYLX_PSEPU P23099:
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                                                                                    XYLX_PSEPU
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us-09-843-250-2.rsp

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MEDLINE=97251358; PubMed=9097040;
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26.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
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STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Maryen J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                SIMILARITY).
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                  SIMILARITY).
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Escherichia.
                                                                                                                                                                                                 52;
                                                                                                                                                              Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                              Mismatches 204; Indels
                                                                                  CON (BY SIMILARITY).

CON (BY SIMILARITY).

CFCC3247A3C4C379 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative dioxygenase alpha subunit yeaw (EC 1.14.1..).
Escherichia coli, and
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IRON-SULFUR (2FE-2S) (B. IRON-SULFUR (2FE-2S) (BY IRON-SULFUR (2FE-2S) (BY IRON (BY SIMILARPTHER) (BY SIMILARPTHER)
                                                                                                                                                          16.5%; Score 398; DB 1; 27.7%; Pred. No. 8.2e-24;
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           95 IR
97 IR
115 IR
118 IR
224 IR
52228 MW;
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               95
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461 AA;
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Dioxygenase;
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P76253;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,

"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00355; Rieske; 1.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; FALSE_NEG.
Hypothetical protein; Oxidoreductase; Iron-sulfur; Iron; Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE-21074933, ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Potanis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
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3.7e-12;
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Pred. No. 3
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EMBL, D90824; BAA15606.1; ALT_INIT.
EMBL, AE005403; AAG56791.1; -.
EMBL, AP002558; BAB35934.1; -.
ECGGENE; EG13509; yeaW.
InterPro; IPR001281; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
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Page 12

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                                                                                                                                                    307
                                                                                                                                                                                                                                                                          281 TVIXEF----PVDSETT-LQNYDIYFTNEELTDEQKSLIEWYRDVFRPEDL---RLVESVQ 333
            HRGKTLVSVEAGNAKGFV-CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARV 141
                                          HRGHQLLSGE-GKAKNVITCPYHAWAFKLDGNLAHARNCENVANFDSDKAQL----VPVRL 146
                                                                      ESFHGFIYGCFDQEAPPLMDYL-GDAAWYLEPM-----FKHSGGLELVGPPGKVVIKANW 195
                                                                                                     ----- ANW 199
                                                                                                                                  KAPAENFVGDAYHVGWTHA--SSLRSGESIFSSLAGNAAL-----PPEGAGLQMTSKYG 247
                                                                                                                                                                                                                         tricolor and its expressions under stress conditions.";
Cell Res. 11:187-193(2001).
-!- FUNCTION: Catalyzes the first step of the osmoprotectant glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: Choline + 2 reduced ferredoxin + O(2) = betaine aldehyde + 2 oxidized ferredoxin + H(2)0.
-:- COFACTOR: Magnesium. Probably binds a 2Fe-2S group and an iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Amaranthaceae; Amaranthus.
                                                                                                                                                                                            SGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                                                       TCSGVFKVWNPIDANTIEVWTY------AIVE--KDM--PEDLKRRLADSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21520075; PubMed=11642403;
Meng Y.L., Wang Y.M., Zhang B., Nii N.;
"Isolation of a choline monooxygenase cDNA clone from Amaranthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF290974; AAK82768.1; -.
InterPro; IPR001281; Rieske.
Pfam; PF00355; Rieske; 1.
Monooxygenase; Oxidoreductase; Chloroplast; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choline monooxygenase, chloroplast precursor (EC 1.14.15.7).
                                                                                          CHLOROPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         442 AA
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TRANSIT 1 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            betaine synthesis.
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334 KGLKSRGY 341
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                                                                                                                                                                                                                                                                                                                                                       KKCLGLKEVARVESFHGFIYGCFDQEAPP----LMDYLGDAAWYLEPMFKHS--GGLEL 182
                                                                                                                                                                                     Gaps
             SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                          210 PKELGLVTL-KVAIWGPFVLISLDRSGSEGTEDVGKEWIGSCA---EEVKKHAFDPSLQF
                                                                                                                                                                                                                      SESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQ
                                                                                                                                                                                     16;
                                                                                                                                                    DB 1; Length 442;
                                                                                                                                                                                     Indels
             IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON (POTEWTAL).
IRON (POTEWTAL).
 CHOLINE MONOOXYGENASE
                                                                                                                                                9.9%; Score 239.5; DB 28.4%; Pred. No. 2.2e-11
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        183 VGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 27, 2003, 08:59:36
Job time: 9.33333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                             : ::||| :|| :| IN-RSEFPMESNWKVFCDNYLDSAYHVPYAH
                                                                                                                                                                                   39;
                                                                                                                 49845 MW;
                                                                                                                                                                                     Conservative
4442
1165
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1187
1290
299
59
165
167
184
187
290
295
442 AA;
                                                                                                                                                                    Similarity
                                                                                                                                                                                     90;
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 Title: Perfect score: OM protein - protein search, using sw model Searched: Sequence: Run on: US-09-843-250-2 2408 1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449 January 27, 2003, 08:55:37; Search time 13.1667 Seconds (without alignments) 3278.305 Million cell updates/sec GenCore version 5.1.3 Compugen Ltd.

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	. 4	ω	2	₽	No.	Result
314.5	334	340.5	390	393	408.5	410.5	417	451	586	588.5	604	616	616	616.5	638	649.5	651.5	724.5	736	736	736	773	956	2055	2291	2345	2403	2403	Score	
13.1	13.9		16.2	16.3	17.0	17.0	7.	æ	24.3	24.4	5	5	Ģ	25.6	٥.	7.	7.	٥.	0	0	30.6	2	9.	85.3	5	97.4	9	99.8	Match	Query
165 T	426	424	464	461	455	454	471	469	458	448	431	458	457	459	461	450	450	455	453	453	453	450	459	447	449	449	462	449	Length	
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T31251	T31278	E83384	G83331	S23477	E83332	A41659	T31281	T50934	JC2467	A29830	3800ML	A42409	JC4993	B41858	S51757	A36516	JN0812	T31258	G85898	D91054	A65031	T31256	T31134	JC5352	C55217	JN0644	S27632	JS0071	ID	
aromatic oxygenase		probable ring-hydr	anthranilate dioxy	probable benzoate	ሥ		benzoate 1,2-dioxy	dioxygenase DitAl,	biphenyl dioxygena	•	œ.	_		_			\vdash		_	_		terminal oxygenase	naphthalene dioxyq	_	Ω		naphthalene 1,2-di	hthalene	Description	

45	44	43	42	41	40	39	38	37	36	ა წ	34	<u>ω</u> ω	32	31	30
186	214.5	223	224	233.5	248	248	248	251.5	267	270.5	283	287	295	311.5	311.5
7.7	8.9	9.3	9.3	9.7	10.3	10.3	10.3	10.4	11.1	11.2	11.8	11.9	12.3	12.9	12.9
426	186	439	446	382	374	374	374	374	420	404	415	412	429	468	468
2	2	N	N	N	N	N	N	N	N	Ν	N	Ŋ	N	N	ν
T08550	JC5354	T09214	T14542	G70946	B64941	G90942	C85791	AF0304	T31285	н87635	AG3320	H95311	F82970	AH2665	G97447
choline monooxygen	2-nitrotoluene dio	choline monooxygen		probable dioxygena	probable choline m	probable choline m	probable choline m	probable dioxygena	biphenyl dioxygena	Rieske 2Fe-2S fami	benzoate 1,2-dioxy	probable aromatic-	probable ring hydr	ring hydroxylating	hypothetical prote

ALIGNMENTS

Qy	Qy Db	Оу Дъ	Qy Db	Qy Db	Qу Db	Qy M	B O 8	#CC 2CC 22	R R R R R R R R R R R R R R R R R R R	RES JSO nap C;S
361 E	301 301	241 241	181 181	121 121	61 61	Matches 1 1	F;81,83,101,104/Binding site: 2Fe-2S cl Query Match 99.8%; Score Best Local Similarity 99.8%; Pred	A; restoues: 1-449 < NOR? A; Cross-references: (B:M23914; NID:g151392; PIDN:AAB4755 C; Comment: Naphthalene dioxydenase system is composed of C; Genetics: A; Gene: ndoB C; Superfamily: toluene dioxygenase terminal oxygenase cc; Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Ries F; 71-119/Domain: Rieske [2Fe-2S] homology < RSK>	R;KurKela, S.; Lehvaeslaiho, H.; Palva, E.T.; Teeri, T.H. Gene 73, 355-362, 1988 A;Title: Cloning, nucleotide sequence and characterization A;Reference number: JS0070; MUID:89211973; PMID:3243438 A;Accession: JS0071 A;Molecule type: DNA A;Molecule type: DNA	RESULT 1 JS0071 JS0071 naphthalene dioxygenase (EC 1.14.12) ndoB protein C;Species: Pseudomonas putida C;Spate: 31-Mar-1992 #sequence_revision 31-Mar-1992 C;Accession: JS0071
DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES 360 	QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 	ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSIRSGESIFSSLAGNAALPPEGAGL 240 	KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 	IDEVIVSRONDGSIRAFLNVCRHRGKTLVSYEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 	448; Conservative 0; Mismatches (1; Indels 0; Gaps 0; MNYNNKILVSESGLSOKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60	Score 2403; DB 2; Length 449; Pred. No. 5.2e-1.84;	three proteins. mponent large chain; ke iron-sulfur protei	, E.T.; Teeri, T.H. and characterization of genes encoding naphthal 973; PMID:3243438	ndoB protein - Pseudomonas putida 31-Mar-1992 #text_change 20-Aug-1999

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R;Denome, S.A.; Stanley, D.C.; Olson, E.S.; Young, K.D. J. Bacteriol. 175, 6890-6901, 1993
A;Title: Metabolism of dibenzothiophene and naphthalene A;Reference number: A49343; MUID:94042852; PMID:8226631 A;Accession: B49343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  naphthalene
C;Species: P.
C;Date: 06-J.
C;Accession:
R;Denome, S.
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A; Rosidues: 14-462 <DE2>
A; Residues: 14-462 <DE2>
A; Cross-references: GB:M60405; NID:g151195; PIDN:AAA16125.1; PID:g294351
A; Experimental source: strain C18
C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; RiC; Superfamily: toluene dioxygenase terminal oxygenase component large chain; RiC; Seywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F; 84-132/Domain: Rieske [2Fe-2S] homology <RSK>
F; 94,96,114,117/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #s
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A; Residues: 1-462 < DEN>
A; Cross-references: EMBL: M60405
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A;Accession: S27632
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Best Local
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                                   421, QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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                                                                                                                 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                  FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
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                    QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                                                                 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWES
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                                                                                    DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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Pred. No. 5.4e-184;
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                J. Bacteriol. 176, 2444-2449, 1994
A;Title: Identification and characterization of A;Reference number: A55217; MUID:94209249; PMID: A;Accession: C55217
                                                                                             polycyclic aromatic hydrocarbon dioxygenase
C;Species: Pseudomonas putida
C;Date: 05-May-1995 #sequence_revision 05-Ma
C;Accession: C55217
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A; Residues: 1-449 <SIM>
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Gene 127, 31-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfur N;Alternate names: nahAc protein C;Species: Pseudomonas putida
A; Status: preliminary
                                                                                 R;Takizawa, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: nahAc
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                                                                               Kaida, N.; Torigoe,
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96.78;
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; Pred. No. 2.2e-179;
10; Mismatches 5;
                                                                                 s.;
                                                                                                                 05-May-1995
                                                                                 Moritani,
                                on of genes encoding PMID:8157615
                                                                                                                                               (EC
                                                                                                                                                 1.14.12.-) iron-sulfur
                                                                                 ₽.;
                                                                               Sawada,
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C;Keywords: 2Fe-2S; heterotetramer; metalloprotein; oxidoreductase; F;71-119/Domain: Rieske [2Fe-2S] homology <RSK> F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (
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tein is a member of naphthalene dioxygenase multicomp
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N, Alternate names: 2-nitrotchuence iron
C;Species: Pseudomonas sp.
C;Date: 27-May-1997 #sequence_revision
C;Accession: JC532
R;Parales, J.V.; Kumar, A.; Parales, R.
Gene 181, 57-61, 1996
A;Title: Cloning and sequencing of the
A;Title: Cloning and sequencing of the
A;Reference number: JC5350; MUID:971287
A;Accession: JC5352
A;Molecule type: DNA
A;Residues: 1-447 <PAR>
A;Cross-references: GB:U49504; NID:g177
A;Experimental source: strain JS42
C;Comment: This enzyme catalyzes the ad
C;Genetics:
A;Gene: ntdAc
C;Superfamily: toluene dioxygenase term
C;Keywords: 2Fe-25; metalloprotein; oxi
F;69-117/Domain: Rieske [ZPe-25] homolo
F;69-117/Domain: Rieske [ZPe-25] homolo
F;79,81,99,102/Binding site: 2Fe-2S Clu
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A; Molecule type: DNA
A; Residues: 1-449 <TAK>
A; Residues: 1-449 <TAK>
A; Cross-references: GB: AB004059; GB: D16629; NID: g2189972; PIDN: BAA20391.1; PID: g391844
A; Cross-references: GB: AB004059; GB: D16629; NID: g2189972; PIDN: BAA20391.1; PID: g391844
C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [21
C; Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F; 71-119/Domain: Rieske [2Fe-2S] homology <RSK>
F; 81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p:
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;79,81,99,102/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (coval
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ce: strain JS42
                 85.3%;
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94.4%;
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     35,
                   Score 2055;
Pred. No. 3
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Pred. No. 4.6e-175;
3; Mismatches 12;
     Mismatches
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                                                                                                                                                                                                        PIDN: AAB40383.1;
                 DB 2;
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                                 Length 447;
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A;Status: preliminary; t)
A;Molecule type: DNA
A;Residues: 1-459 <ROM>
A;Cross-references: EMBL;
C;Genetics:
                                                                                                                                                                                                                                                                                             A;Gene: bphAlf
A;Gene: plasmid pNLl
A;Genome: plasmid pNLl
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protei
F;80,82,100,103/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; submitted to the EMBL Data Library, July 1999 A;Description: Complete sequence of a 184 kb A;Reference number: Z20992 A;Accession: T31134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                naphthalene dioxygenase (EC 1.14.12.-) large chain - Sphingomonas aromaticivorans C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000 C;Accession: T31134
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Best Local S
Matches 192
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                                                                                                RQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGES
                                                                                                                                                  LVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVS
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                                                                          RQPDGSLKAFINSCTHRGNQICHADSGSAKAFVCNYHGWVFGQDGSLVDVPMEERCYHSD
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LDKSKLGLAPI-RVETYKGFIFGCHDPEAPSLEDYLGDFCWYLDTIWDGPDGGLELLGPP
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192; Conser
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C; Superf
C; Keywor
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C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #tex
C;Accession: T31256
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston,
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic
A;Reference number: 220992
A;Accession: T31256
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A; Residues: 1-450 < ROM>
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Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein;
81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
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LFDNDDGDNLTACTEQSRGWRTAQMDVYTNMALGRSGKREG-FPGDIAAGLVSEHNQRYF
                                                                         NITIFPNLQLLPGLNWFRVYHPKGPGQIEQWTWAMAENDMPEAVKAQILENQCLTFGLAG
                                                                                                  NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAG
                                                                                                                                                                                                                                   SALLGETQKMVLGTNWKLPVENVCGDGYHLGWAHAGAMAAVQSMDLTGLSVGNSGVDLDG
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A; Residues: 1-19, 'A', 21-383, 'ATAPATANCVWKW', 397-398, 451, 'R', 453, 'SAATTAFLALLTISFQKLPL
A; Cross-references: EMBL: Z37966; NID: g550595; PIDN: CAA86018.1; PID: g550596
C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C; Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
C; Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
E; 75-123/Domain: Rieske [2Fe-2S] homology <RSK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: strain K-12, substrain MGI655 R;Turlin, E.; Gasser, F.; Biville, F. submitted to the EMBL Data Library, September 1994 A;Description: Cloning and sequencing of an E. coli gene homologous to A;Reference number: S49292 A;Accession: S49292
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.A.; Rose, D.J.; Mau, B.; Shao,
Science 277, 1453 1462, 1997
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                                             YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                           GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS 412
                                                                                                                                                                                         AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
                                                                                                                                                                                                                                            RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTV
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                                                                                                                                                                                                                                                                                                                                                                                            AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD-----
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A;Gene: ECs3
C;Superfamil:
C;Keywords:
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biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2001 C; Accession: G85898
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, liller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                   iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E., Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85898
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biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2001
C; Pacession: D91054
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, F.
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, F.; Hartori, M.; Shinadawa, F.
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A;Residues: 1-453 <HAY>
A;Residues: 1-453 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36827.1; PID:913362875;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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Molecule type: |
| Residues: 1-453
                                   Status: preliminary
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Shiba, T.;
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aromatic oxygenase large chain - Sphingomonas aromaticivorans plasmid pNL1 (C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000 C;Accession: T31258 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Ser submitted to the EMBL Data Library, July 1998 A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingom A;Reference number: Z20992 A;Accession: T31258 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-455 <ROM>
                                                                                                                   A.Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378399; PIDN:AAD03982. C:Genetics:
A.Genome: plasmid pNL1
A.Genome: plasmid pNL1
A.Genome: phasmid pNL1
C:Superfamily: toluene dioxygenase terminal oxygenase component large chain; C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
C:Reywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
C:Reywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
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C; Superfamily: toluene dio:
C; Keywords: oxidoreductase
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DYSRYMDLKEGWLDRR--IFSDADIYEEELYRIFARSWLFVAHESQIPSSGDFLTTHMGE

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A;Cross-references: GB:L04642; GB:L04643; NID:g6552505; PIDN:AAA17758.1; PID:g309855
A;Experimental source: strain ML2
C;Comment: This enzyme is involved in catalyzing the oxidation of benzene to cis-1,2-dil C;Comment: The reduced enzyme catalyzes the oxidation of benzene to cis-benzene dihydroc C;Genetics:
A;Gene: bedC1
A;Genome: plasmid
A;Genome: plasmid
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [2F6 C;Keywords: 2Fe-25; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; Rif F;86-134/Domain: Rieske [2Fe-25] homology <RSK>
F;96,98,116,119/Binding site: 2Fe-25 cluster (Cys, His, Cys, His) (covalent) #status professional control of the control of th
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C:Date: 19-May-1994 #sequence_revision 06-Jan-1995 #text_c
C:Accession: JNO812
R:Tan, H.M.; Tang, H.Y.; Joannou, C.L.; Abdel-Wahab, N.H.;
Gene 130, 33-39, 1993
A;Title: The Pseudomonas putida ML2 plasmid-encoded genes
A;Reference number: JNO810; MUID:93345820; PMID:8344526
A;Accession: JNO812
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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Date: 19-May-1994 #sequence_revision 06-Jan-1995 #text_change
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WKAPAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
                                                                                          --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                      VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
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                                              PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
                                                                                                                                                                                                                                                                                      IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
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                                                                                                                                             QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA-----
                                                                                                                                                                                                                                        IYTDEDLYQLELERVFARSWLLLGHETHIRKPGDYFTTYMGEDPVVVVRQKDASIAVFLN
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                                                                                                                                                                                                                                                                                                                                                             34.6%;
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                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.1e-44; 
); Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                   Score 651.5;
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C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske C;Keywords: 2\text{Fe}-2\text{S}; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; F;86-134/Domain: Rieske [2\text{Fe}-2\text{S}] homology <RSK> F;96-98,116,119/Binding site: 2\text{Fe}-2\text{S} cluster (2\text{Cys}, His, 2\text{Cys}, His) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Pseudomonas putida
C:Date: 15-reb-1991 #sequence_revision
C:Accession: A36516
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A; Residues: 1-450 <ZYL>
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A; Title: Toluene degradation
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                                                                                                                                                                 GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
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                                                                    PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
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                                                                                                                 TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWESDDNDNME
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MUID:89359301; F
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PMID:2670929
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submitted to the EMBL Data Library, July 1994
A; Description: Evolutionary relationship of the biphenyl dioxygenase of the A; Reference number: S51757
A; Accession: S51757
A; Molecule type: DNA
A; Residues: 1-461 <AST>
A; Cross-references: EMBL:X80041; NID:g607171; PIDN:CAA56346.1; PID:g607172
A; 
RESULT 15
B41858
biphenyl dioxygenase (EC 1.14.12.-) terminal oxygenase component large chain c;Species: Pseudomonas sp.
C;Date: 04-Mar-1993 #sequence_revision 06-Jan-1995 #text_change 05-May-2000 C;Accession: B41858
R;Erickson, B.D.; Mondello, F.J.
J. Bacteriol. 174, 2903-2912, 1992
A;Title: Nucleotide sequencing and transcriptional mapping of the genes encoder.
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551757

biphenyl dioxygenase (EC 1.14.-.-) large chain - Rhodococcus globerulus
C;Species: Rhodococcus globerulus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S51757
C;Accession: S51757
R;Asturias, J.A.; Diaz, E.; Timmis, K.N.
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A;Reference number: A41858; MUID:92234948; PMID:1569021
A;Accession: B41858
A;Molecule type: DNA
A;Residues: 1-459 < CERI>
A;Residues: 1-459 < CERI>
A;Cross-references: GB:M86348; NID:g349602; PIDN:AAB63425.1; PID:g151084
A;Experimental source: strain LB400
A;Experimental source: strain LB400
A;Cotes: Sequence extracted from NCBI backbone (NCBIN:97256, NCBIP:97259)
C;Genetics:
A;Gene: bphA1; bphA
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Keywords: 2Fe-25; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase;
F;90-138/Domain: Rieske [2Fe-25] homology <RSK>
F;100,102,120,123/Binding site: 2Fe-25 cluster (Cys, His, Cys, His) (covalent) #statu
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                                            AIGETSYRGFYRAYQAHVSSSNWA
                                                                                                HNIRNFSAGGVFEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y
                                                                                                                                                                                                VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR
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VYAEEAARGMYHHWMRMMSEPSWA
                                                                                                                                            SVQRTVGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKS
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32.9%;
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Pred. No. 2.7e-41;
9; Mismatches 186;
  455
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Database
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Maximum Match 10
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Maximum DB seq length: 2000000000
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A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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2408
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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99.7	99.8	99.8	99.8	99.8	99.9	100.0	100.0	100.0	100.0	Query Match
449	449	449	449	449	449	449	449	449	449	Length
21	21	21	21	21	21	21	21	21	21	DB
AAB12578	AAB12577	AAB12568	AAB12580	AAB12579	AAB12581	AAB12582	AAB12567	AAB12566	AAB12565	ID
Naphthalene dioxyg	Naphthalene dioxyq	NDO related comple	Naphthalene dioxyq	Naphthalene dioxyq	Naphthalene dioxyq	Naphthalene dioxyq	NDO related comple	NDO related comple	Naphthalene dioxyq	Description

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405	35	35	35	1193	426	99	439	446	438	433	433	435	424	497	385	490	427	458	458	459	443	898	453	452	451	447	447	449	449	449	449	449	448	449
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AAW80332	90	AAW79019	10	ABG18089	316	ABP35375	AAW69562	AAW69563	ABB06798	AAG62635	AAG62633	AAG62634	AAU33601	AAB79227	AAU36099	AAG92386	AAR32085	AAY81989	AAY81990	AAR66729	AAO17350	AAY83939	AAU34660	947	AAB12576	57	57	S.	57	57	257	25		AAB12583
Oxidase amino acid	'n	moti	motif ;	Novel human diagno	Herbicidally activ	Human oxygenase-li	유	et cholin	hortens	choline		C album choline mo	Pseudomonas aerugi	Corynebacterium gl	Klebsiella pneumon	C glutamicum prote	dioxy	Chimeric PCB decom	Chimeric PCB decom		ctero	nzene ring hydr	coli cell	*	related	related		related	related	related	related	comp1	dioxy	Naphthalene dioxyq

ALIGNMENTS

PT	DR DR	XX	ΡI	×	PA	PR	×	PF	×	B	×	PN	X C	S 6	202	X X	X	KW	XX	DE X	DŢ	XX	AC A	ID	AAB1	RESILT
Novel naphthalene dioxygenase mutant having a specific amino acid	WPI; 2000-452174/39. N-PSDB; AAA65339.		Parales R, Gibson D, Resnick S, Lee K;		(IOWA) UNIV IOWA RES FOUND.	26-OCT-1998; 98US-0105575.		26-OCT-1999; 99WO-US25079.		29TITN - 2000		WO200037480-A1			Pseudomonas sp.	polymer; resin; pharmaceutical; rubber industry; bioremediation.	inducible multi-component enzyme; alpha subunit; mutant; chiral diol;	Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO;		Naphthalene dioxyqenase mutant F352V protein sequence SEO ID NO:2.	09-NOV-2000 (first entry)		AAB12565;	AAB12565 standard; Protein; 449 AA.	AAB12565	17.77

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroy3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
 AAB12566 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1S.2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S.2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes a naphthalene dioxygenase (NDO) or Nated complex (I) comprising several polypeptides which contain an
                                                                                     QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                             DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                      QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG
                                                                                                                      QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                           FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
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                                                                                                                                                                                                                                                               FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                                                                                                                                                                                                                    QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                       ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
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Protein; 449
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                                                                                                                                                                                                                                                                           CC alpha subunit that contains substituted amino acids at specific consistions. The polypeptides and host cells are useful for preparing cc (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-cc dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-cc dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cc involves contacting them with naphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydronaphthalene respectively. The polypeptides and ct the host cells are also useful for preparing 1,2-dihydroxy-1,2-cc dihydroxy-naphthalene or 3,4-dihydroxy-3,4-dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which constructing them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an cromatic compound such as indene, 1,2-dihydronaphthalene, dibenazofuran, cc dibenazothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cc cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cc exemplification of the present invention.
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a naphthalene dioxygenase (NDO) of related complex (I) comprising several polypeptides which contain alpha subunit that contains substituted amino acids at specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 99-100; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; ND inducible multi-component enzyme; alpha subunit; mutant; chiral polymer; resin; pharmaceutical; rubber industry; bioremediation
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Pred. No. 4e-225;
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The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1S, 2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S, 2R)-cis-phenanthrene-1,2-dihydronaphthalene, which dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which
                                                                                                                                                                                                                              Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                       Claim
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polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDO related complex alpha subunit protein sequence SEQ ID NO:15.
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Matches 449
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                                                                                                                                     Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDC inducible multi-component enzyme; alpha subunit; mutant; chiral polymer; resin; pharmaceutical; rubber industry; bioremediation
                                                                                                                                                                                                                                                                                                AAB12582 standard;
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                                                                                                         Pseudomonas
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26-OCT-1999; 29-JUN-2000

99WO-US25079

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CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydronaphthalene, respectively. The polypeptides and CC the host cells are also useful for preparing 1,2-dihydroxy-1,2-CC involves contacting them with phenanthrene. The polypeptides and the CC involves contacting them with phenanthrene. The polypeptides and the CC host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, CC dibenzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, CC acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, CC dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a CC corresponding dihydro dihydroxy compound. The polypeptides and the host C cells are useful for preparing chiral diols for use in the polymer, CC anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted annotating several positions. The polypeptides and host cells are useful for preparing (-)-(1S,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,2-dihydrodiol
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         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                      QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
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       Page 128-129; 151pp; English
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RESULT 7 AAB12580

AAB12580 standard;

Protein;

EXXEX DXX

(first entry)

09-NOV-2000 (f.
Naphthalene dio:
Pseudomonas sp.

dioxygenase mutant F352T protein sequence SEQ ID

NO:34

strain NCIB 9816-4; naphthalene dioxygenase;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (1) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)-(15.2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-CC dihydroxyindan, 1.2-dihydroxy-1.2.3,4-terrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, clidhydroxyindan, 1.2-dihydronaphthalene, perparing 1.2-dihydroxy-1.2-CC dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy-1.2-dihydroxy
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                                                                                                       DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                       FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                                                                                                                                                                                                                                                       IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                     QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARI,YRSHLNCTV
                                                                                                                                                                                                                                                                           QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                               DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                   FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bloremediation in which they oxidise an
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polymer; resin; pharmaceutical; rubber industry; bioremediation.
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                                          ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                  ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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                                                               The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-cihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-cihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indeme, and 1,2-dihydronaphthalene biphenyl, phenanthrene, cindeme, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-3,4-dihydroxy-1,2-dihydrophenanthrene also used in bioremediation in which they oxidise an aromatic compound such as indeme, 1,2-dihydronaphthalene, and 1,3-dihydronaphthalene, and 1,3-dihydronap
benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 102-103; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia
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N-PSDB; AAA65342.
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                                                                                           DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 AA;
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Pred. No. 1.2e-224;
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                                                                                                                                                                                                                                                                                                                       dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which convolves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-cdihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which convolves contacting them with phenanthrene. The polypeptides and the host cells are also used in bloremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, caenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, caenaphthylene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the care was a compound.
                                                                                                                                                                               Matches
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Best Local
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                       IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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                                                                                                                                                                                                                                                                                  449
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                                                                                                                Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
                                                                                                                                                                                                                                                                                                                         Pseudomonas
Synthetic.
                                                                                                                                                                                            Parales R, Gibson D,
                                                                                                                                                                                                                                       26-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB12583;
                                                                                                                                                                                                                                                           26-OCT-1999;
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                                                                                                                                                                                                                                                                                                    WO200037480-A1
                                                                                                                                                                                                                                                                                                                                                        polymer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB12583
                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                  Naphthalene
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DB; AAA65376.
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                                                                                                                                                                                                                                                                                                                                                         resin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                       multi-component enzyme; alpha
resin; pharmaceutical; rubber i
                                                                                                                                                                                                                                                                                                                                   gp
                                                                                                                                                                                                                                                                                                                                                                                                dioxygenase mutant F352W
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industry;
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e polymer, resin,
t bioremediation
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The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted and subunit that contains substituted along access at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,2-dihydrodio

1,2-dihydroxy-1

,2,3,4-tetrahydronaphthalene,

Example 7; Page 142-144; 151pp;

English.

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RESULT 1:
AAB12584
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                                                                      Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral dipolymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                        AAB12584 standard;
                                           Pseudomonas
                                                                                                                                      Naphthalene dioxygenase mutant F352Y protein sequence SEQ
                                                                                                                                                                          09-NOV-2000
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                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                        Protein;
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Pred. No. 1.9e-224;
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Matches Best

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1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG

MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG

60 60

IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120

Local Similarity

Conservative

0;

Mismatches

Indels

0;

Gaps

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FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES

FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTYGPAGFWES

300 300 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL

ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL

240 240 180 180

KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE

181 181 121 121 61 61

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CC alpha subunit that contains substituted amino acids at specific copositions. The polypeptides and host cells are useful for preparing cc (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-cc dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-cc dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cc involves contacting them with naphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydronaphthalene respectively. The polypeptides and ct the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydrophenanthrene which compound such as indene, 1,2-dihydronaphthalene, which chost cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, cc dibenzocthiophene, 9,10-dihydronaphthalene, dibenzocfuran, cc dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a ccorresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cc exemplification of the present invention.
                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a naphthalene dioxygenase (NDO) or related complex (I) comprising several polypeptides which contain
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-2000
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                                                                  448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibson D,
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99.6%;
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Score 2398; DB 21; Pred. No. 3.7e-224;
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                      DB 21;
                    Length 448;
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В δÃ

Query Match Best Local :

Local Similarity

99.6%;

Length 449;

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RESULT 13
AAB12569
ID AAB12
dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-themathrene or 3,4-dihydroxy-3,4-dihydroxy-themathrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, oxidise an benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cesin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the care exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 104-105; 151pp; English.
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Sequence

Novel naphthalene dioxygenase mutant having a specific amino substitution for preparing chiral diols for use in the polyme pharmaceutical or rubber industry and for carrying out biorem

polymer, resin, bioremediation

acid

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RESULT 14
AAB12570
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                                                   WPI; 2000-452174/39
                                                                                                                  26-OCT-1998;
                                                                                                                                                            29-JUN-2000
                                                                                                                                                                                                                                   Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral cipolymer; resin; pharmaceutical; rubber industry; bioremediation.
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                                                                                                                                                                                                                                                                                                                                              AAB12570 standard; Protein; 449
                                                                                           (IOWA ) UNIV
                                                                                                                                      26-OCT-1999;
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                                                                                                                  98US-0105575
                                                                                                                                       99WO-US25079
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Pred. No. 3.8e-224;
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cc alpha subunit that contains substituted amino acids at specific cc positions. The polypeptides and host cells are useful for preparing cc (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-cc dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydronaphthalene, which cc involves contacting them with naphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydronaphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydronaphthalene respectively. The polypeptides and cc involves contacting them with naphthalene, biphenyl, phenanthrene, and involves contacting them with phenanthrene. The polypeptides and cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which cc involves contacting them with phenanthrene. The polypeptides and the cc host cells are also used in bioremediation in which they oxidise an cc aromatic compound such as indene, 1,2-dihydronaphthalene, cells are also used in bioremediation in which they oxidise an cc aromatic compound such as indene, 1,2-dihydronaphthalene, cc acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, cc dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a cc corresponding dihydro dihydroanthracene, or 9,10-dihydrophenanthrene a cc corresponding dihydro rubber industry. The present sequence represents cells are useful for preparing chiral diols for use in the polymer, cc anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the cc exemplification of the present invention.
                                                                                             RESULT 15
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  09-NOV-2000
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435; Conserv
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                                                                            standard;
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(first entry)
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                                                                            Protein; 449
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L.7e-219;
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                                                                                                                                                           Query Match
Best Local S
Matches 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 107-109; 151pp; English
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                                                                                                 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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                   IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                             MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIXARNWLFLTHDSLIPSPGDYVTAKMG
                                                                                                                                                             430;
                                                                                                                                                           Similarity 95.1
30; Conservative
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pharmaceutical; rubber industry; bioremediation.
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e polymer, resin,
t bioremediation
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the
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ОУ	Db Qy	Db dg	ду	dg Qy	Db dd
421 421	361 361	301 301	241 241	181 181	121 121
QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 	DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 	FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES 360	QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 - - - - - - - - - - - - - - - - -	ELVGPPGKVVIKANWKAPAENFYGDAYHYGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 	KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
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Search completed: January 27, 2003, 08:58:45 Job time : 31.1667 secs



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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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Published_Applications_AA:*

1: //gqn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: //gqn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: //gqn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: //gqn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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7: //gqn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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Gapop 10.0 , Gapext 0.5
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2410
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. 1 2 3 3 4 4 6 6 7 7	Score 734 377.5 378.5 185 185 174 174	Query Match 30.5 15.7 15.6 13.8 7.7 7.7 7.2 7.2	Query Query Match Length 30.5 453 315.7 385 115.6 490 13.8 424 7.7 35 7.7 35 7.2 35 7.0 35	DB 10 10 10 10 10 10 10 10 10 10 10 10 10	ID US-09-815-242-10253 US-09-815-242-11692 US-09-738-626-6140 US-09-776-490-19 US-09-776-491-19 US-09-776-491-20 US-09-776-491-20 US-09-776-490-21 US-09-776-490-21 US-09-776-490-21	Sequence 10253 Sequence 11692 Sequence 6140, Sequence 5097, Sequence 19, Al Sequence 20, Al Sequence 20, Al Sequence 21, Al Sequence 21, Al
4ω	376 333.5	15.6 13.8	490 424	10	US-09-738-626-6140 US-09-815-242-5097	Sequence 51
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6	185	7.7	35	10	US-09-776-491-19	Sequence 1
7	174	7.2	35	10	US-09-776-490-20	Sequence 2
8	174	7.2	35	10	US-09-776-491-20	Sequence 2
9	168	7.0	35	10	US-09-776-490-21	Sequence 2
10	168	7.0	35	10	US-09-776-491-21	Sequence 21
11	118.5	4.9	354	ب	US-08-976-063C-4	Sequence 4,
12	110	4.6	35	10	US-09-776-490-12	Sequence 1
13	110	4.6	35	10	US-09-776-491-12	Sequence 1
14	109	4.5	u S	10	US-09-776-490-14	Sequence 1
15	109	4.5	35	10	US-09-776-491-14	Sequence 1
16	108	4.5	35	10	US-09-776-490-13	Sequence 1
17	108	4.5	35	10	US-09-776-490-15	Sequence 1
18	108	4.5	35	10	US-09-776-491-13	Sequence 1
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3.9	3.9	3.9	3.9	3.9	3.9	4.0	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4 .3	4.3	4.3	4.3	4.3	4.4	4.4	4.5
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US-09-995-542-9	US-09-776-491-16	US-09-776-490-16	US-09-925-301-1362	US-09-776-491-46	US-09-776-490-46	US-09-712-363-246	US-09-776-491-17	US-09-776-490-17	US-09-776-491-45	US-09-776-491-44	US-09-776-490-45	US-09-776-490-44	US-09-738-626-6115	US-09-776-491-10	US-09-776-491-8	US-09-776-490-10	US-09-776-490-8	US-09-776-491-11	US-09-776-490-11	US-09-776-491-18	US-09-776-490-18	US-09-924-097-15	US-09-776-491-9	US-09-776-490-9	US-10-047-542-78
Sequence 9, Appli		Sequence 16, Appl	Sequence 1362, Ap	46	Sequence 46, Appl	•	Sequence 17, Appl	Sequence 17, Appl	•	Sequence 44, Appl		Sequence 44, Appl	Sequence 6115, Ap	Sequence 10, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 11, Appl	Sequence 11, Appl	18,	Sequence 18, Appl	Sequence 15, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 78, Appl

ALIGNMENTS

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                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 11692 LENGTH: 385
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PRIOR
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                            PRIOR APPLICATION | PRIOR FILING DATE:
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                            NUMBER OF SEQ ID NOS:
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  ORGANISM: Klebsiella
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                                                                                                                              APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                      APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PEGAGLOMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVESYKGLIFGNWDTSAPGLRDYLGDIAWYLDGMLDRREGGTEIVGGVQKWVINCNWKFP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTG 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEXDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYTDPDIYQLELERIFGRCWLFLAHESQIPKPGDFFNTYMGEDAVVVVRQKDGSIKAFLN 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6140
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                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                     SEQ ID NO 6140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6140, A Publication No.
                                                                                                                                             Query Match
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Best Local Similarity
                                                                                                          Matches
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059 SOFTWARE: Patentin ver. 3.0
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                                                               IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
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VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKD-LYGESLNKK-CLGLKE 137
                                   IFTDPEIFELEMRHIFEGNWIYLAHESQIPNAGDYFTTYIGRQPIMITRSKDGTLNCLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTTEV--WTYAIV-EKDMPEDLK-RRLAD--SVQRTGGPAGFWESDDNDNME--TASQNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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ANDO, SEIKO
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                                                                                                          Conservative
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                                                                                                          15.6%; Score 376; DB 9; 26.7%; Pred. No. 1.1e-25; tive 66; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                  Pred. No. 1.1e
6; Mismatches
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                                                                                                                               ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5097
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                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5097, Application Patent No. US20020061569A1
                                             Matches
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                        TYPE: PRT
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    25
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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  ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGLYPIQHGFWHELMQEAVNKQSIKEKELADDT 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLK----RRLADSVQRTGGPAGFWESDDND 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APAENFVGDAYHVGWTH-----ASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGFY-----RAYQAHVSSSNWAEFEHASST 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLEEFRSCQKTYQASAFPWNDM--TRGLGHQVQG----PNEVAKGLGMNEVLSSGARTED 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSSQIRHIRPISVDQTEVTIYCIAPKGESAEARANRIRQYEDFFNATG-----MATPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto, Robert T
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grant J
                                                                                                                                                                                                                                                                           2001-02-16
                                                                13.8%;
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                                             70;
                                        Score.333.5; I
Pred. No. 5.6e.
70; Mismatches
                                      i.6e-22;
nes 178;
                                                                                    DB 10;
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                                           Indels
                                                                                 Length
                                                                                    424;
                                           55;
                                        Gaps
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                                                                                                   TELEX: 575102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 EILESCO---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 DNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 -VYRNFLFIHYGARQASLETYLGQAKDYIDLICDQSEAELEIIPGGFEHSIKANWKLLAE 199
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APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: CURRENT
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/810,009
ETILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
MOLECULE TYPE: protein
                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 28234
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISGPPSTGRPIAYWSPLFPEALKPSIAAKFERLVERFGQARAEDIAHTNKSLFIFPNLVI 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                      STRANDEDNESS: <Unknown>
                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Charlotte STATE: No. US20010012886Alth Carolina
                                                                               LENGTH: 35 amino acids
                                                                                                                                                                 TELEFAX: 919-881-3175
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Drawer 34009
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                     linear
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                                                                                                                                                                                                                                5718-4
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US-09-776-491-19
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Sequence 20, Application US/09776490 Patent No. US20010012886A1
                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                             TELEX: 575102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                             Local Similarity 94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Uknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLAI
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BELL, 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte STATE: No. US20010013135Alth Carolina
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                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                            LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            ELEFAX: 919-881-3175
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ilarity 94.3%;
Conservative
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Pred. No. 2.7e-10;
1; Mismatches 1;
                                                                                                                                                                            Score 185; DB 10;
Pred. No. 2.7e-10;
                                                                                                                                                               Mismatches
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                                                                                                                                                                                                DB 10;
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                                                                                                                                                                                             Length 35;
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                                                                STATE: NO.
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-776-490-20
                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
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Best Local Similarity 85.7%;
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
Gray, John
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         CELL DEATH AND DISEASE RESISTANCE NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
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                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                    ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                             COUNTRY: USA
ZIP: 28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                               Johal, John
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                                                                                       US20010013135A1th Carolina
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Pred. No. 2.5e-09;
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                                                                                                                                                 PARK & GIBSON
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

OPERATING

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US-09-776-490-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/09776490
Patent No. US20010012886A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        μ,
                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLAI
                                                                          APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION: NAME: Spruill, W. Murray
                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BR PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 20:
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                   TELECOMMUNICATION INFORMATION:
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                                     NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943 REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                   APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Charlotte STATE: No. US20010012886Alth Carolina
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TELEFAX: 919-881-3175
TELEX: 575102
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FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
TELEPHONE: 919-881-3140
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85.7%;
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Pred. No. 2.5e-09;
2; Mismatches 3;
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TOPOLOGY: Inear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-776-491-21
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US-09-776-491-21
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 Query Match 7.0%;
Best Local Similarity 80.0%;
Matches 28; Conservative
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Patent No. US20010013135A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21:
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TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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ADDRESSEE: BELL, S
STREET: P.O. Drawe
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                  STRANDEDNESS: <Unknown>
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TELEFAX: 919-881-3175
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Score 168; DB 10;
Pred. No. 8.7e-09;
3; Mismatches 4
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Pred. No. 8.7e-09;
3; Mismatches 4
                                       DB 10;
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                                   Length 35;
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Gaps
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US-08-976-063C-4
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MEDIUM TYPE: DISKette, 3.50
COMPUTER: HP VECTRA
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bay
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alexander Steinbuchel: Horst Priefert; Jurgen Rabenhorst TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF TITLE OF INVENTION: CONIFERYLALDEHYDE, FERULIC AVITITLE OF INVENTION: ACID AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 196 4
FILING DATE: 29-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: 'Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
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FILING DATE: 21-NOV-1997
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                                                                                                                 ENFVGDAYHVGWTHASSLR-----
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                                                                                                                                                                                         SFHGFIY---GCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPA 199
                                                                                                                                                                                                                               ----SLGFVRDGKLICGYHGLEMGCEGKTLAMP------GQRVQGFPCIKSYA-VE 99
                                                                                                                                                                                                                                                                                                        MFPKNAWYVACTPDEIADKP---LGROICNEKIVFYRGPEGRVAAVEDFCPHRGAPL---
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 208
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amino acid
OGY: linear
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RESULT 13
US-09-776-491-12
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US-09-776-490-12
                                                                                                                                                                                      Sequence 12, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
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nes 18; Conserv
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTZER,
STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                APPLICANT: Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Charlotte STATE: No. US20010012886Alth Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                               Johal, Gurmukh S. Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28234
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Johal, Gurmukh S.
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                                                                                   CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 110; DB 10;
Pred. No. 0.0013;
4; Mismatches 12;
                       PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARK & GIBSON
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RESULT 14
US-09-776-490-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. US20010012886A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NQCRHRGMRICRADAGNAKAPTCSYHGWAYDTAG 34
                                                                                                                     ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                  APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 919-00-
17 FFAX: 919-881-3175
                                                                                                                                                                                                                                                                                            CITY: Charlotte STATE: No. US20010012886Alth Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
          APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Charlotte STATE: No. US20010013135A1th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09776490
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US-09-776-491-14
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Patent No. US20010013135A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                  INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.5%;
Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NQCRHRGMRICRADGGNAKSPTCSYHGWAYDSAG
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 28234
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SPILLII, W. MULTSY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray, Jo. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                                        NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/776,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Charlotte STATE: No. US20010013135Alth Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELTZER, PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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Pred. No. 0.0016;
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13;

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Length 35; Indels

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Overy Match
Overy Match
Best Local Similarity 4.5%; Score 109; DB 10; Length 35;
Best Local Similarity 52.9%; Fred: Mo. 0.0016;
Best Local Similarity 52.9%; Fred: Mo. 0.0016;
Best Local Similarity 52.9%; Fred: Mo. 0.0016;
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Over Match
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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                              Scoring table:
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262574 seqs, 29422922 residues
                                         Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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94.5	95	95	99	99	99.5	100	101	101	102	102	103	104	105.5	105.5	106	108	108	108	109	110	113.5	168	174	185	223	224	Score		
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US-08-828-922-1	US-09-134-001C-4800	1 US-08-810-009-46	3 US-08-812-829-6	3 US-08-814-052-6	9327	-600	us-08-810-009-45	US-08-810-009-44	US-08-810-009-10	us-08-810-009-8	US-08-810-009-11	-08-810-009-1	US-08-809-326A-15		us-08-810-009-9	US-09-311-626B-4	-600	Ļ	US-08-810-009-14		3 US-09-028-934-36	us-08-810-009-21	US-08-810-009-20	us-08-810-009-19	1 US-09-004-393B-2	I US-09-004-393B-4	3 ID		
Sequence 1, Appli	4800, A	46	ο	6, 2	57,		45,	44,	10,	8, 2	11,	18,	15,	16,	9	4,	15,	13,	14,	12,	Sequence 36, Appl	21,	20,	19,	2,	Sequence 4, Appli	Description		

RESULT 2
US-09-004-393B-2
IS-09-004-393B-2
; Sequence 2, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
; APPLICANT: Hanson D., Andrew

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997	774	774	774	346	345	471	750	750	525	525	1358	1087	1087	421	35	5588	5588	
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US-08-232-540-1	US-09-702-572-7	US-09-448-076-7	US-09-276-400-7	US-09-149-476-493	US-09-362-123A-2	US-08-914-375C-70	US-08-812-829-2	US-08-814-052-2	US-08-905-817-2	US-08-348-891A-2	US-08-570-311-27	US-08-353-485-8	US-08-570-311-8	US-09-239-303-2	US-08-810-009-16	US-09-370-700-6	US-09-036-987A-6	
Sequence 1, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 493, App	Sequence 2, Appli	Sequence 70, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 27, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 6, Appli	Sequence 6, Appli	

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                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09004393B Patent No. 6310271 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: UF-162
CURRENT APPLICATION NUMBER: US/09/004,393B
CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/035,147
PRIOR FILING DATE: 1997-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 446
TYPE: PRT
ORGANISM: Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
275 F-----PMECNWKVFCDNYLDSSYHVPYAH 299
                                  182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                          216
                                                                                                         131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMD----YLGDA-----AWYLEPMFKHSGGLE 181
                                                                                                                                              159 QGELHAFHNVCTHRA-SILACGSGKKSCFVCPYHGWVYGLDGSLAKA--SKATETQNLDP 215
                                                                                                                                                                                71 DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                     99 EDALTPPSTWYTEPAFYSHELERIFYKGWQVAGYSEQVKEKNQYFTGSLGNVEYLVSRDG 158
                                                                                                                                                                                                                                        11 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMGIDEVIVSRQN 70
                                                                   58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson D., Andrew
Rathinasabapathi, Bala
Burnet, Michael
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                          9.3%; Score 224; DB 4
27.4%; Pred. No. 2e-13;
ative 37; Mismatches
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US-08-810-009-19
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; ORGANISM: Spinacia oleracea
US-09-004-393B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6211437
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/004,393B CURRENT FILING DATE: 1998-01-08 PRIOR APPLICATION NUMBER: 60/035,147 PRIOR FILING DATE: 1997-01-08 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burnet, Michael TITLE OF INVENTION: Polynumitte OF INVENTION: Plants FILE REFERENCE: UF-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Johal, Guri
APPLICANT: Gray, John
              TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 FQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYLDSSYHVPYAH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVLISLDRSLEEGGDVGTEWLGTSA---EDVKAHAFDPSLQFI-HRSEFPMESNWKIFSD 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SILACGSGKKSCFVCPYHGWVYGMDGSLAKASKAKP--EQNLDPKELGLVPL-KVAVWGP 223
                                                                                                                                                                                                                                                                                                                      2823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Briggs, Steven P. Johal, Gurmukh S.
919-881-3175
                                                                                                                                                                                                                                                                                                                                         USA
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                                                                 32,943
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                                                         5718-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 223; DB 4;
Pred. No. 2.5e-13;
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                                                                         Query Match
Best Local.
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Patent No.
                                                           Matches
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                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPHAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Briggs, Steven
APPLICANT: Johal, Gurmukh
APPLICANT: Gray, John
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                TELLEFAX: >1.
TELEFAX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.V. STREET: P.V. CITY: Charlotte
CITY: Charlotte
STATE: NO. 6211437th Carolina
                                                   7.2%;
Local Similarity 85.7%;
les 30; Conservation
                          79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK
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94.3%;
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                                                        Score 174; DB 4
Pred. No. 3e-10;
2; Mismatches
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Pred. No. 2.6e-11
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 35
                                                                                      DB 4; Length 35;
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RESULT 5 US-08-810-009-21

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Patent No. 6211437
Patent INFORMATION:
"" Briggs,
                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                         Sequence 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                        TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                APPLICANT:
                                                                                        CORRESPONDENCE ADDRESS
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
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CORRESPONDENCE ADDRESS:
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APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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CTTY: Charlotte
62114
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TELEFAX: >--
TEX: 575102
                                            STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
   COUNTRY: UZIP: 27709
                                 STATE: NC
                                                             ADDRESSEE: No. 6117670artis Corporation STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                   1 NVCRHRGKTIVDAEAGNAKGPVCGYHGWGYGSNGK 35
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5. 6211437
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 28; Conserv
                                                                                                                                                                                                                                                                            5, Application US/09028934 6117670
                                                                                                                                                                                                             Ligon, James M.
Hill, Dwight S.
Lam, Steven T.
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                                                                                                                                                    Kirner, Sabine
Young, Thomas R.
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                                                                                                                                                                                               Hammer, Philip E.
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3ER: 5718-4
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Pred. No. 1.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
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APPLICANT:
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RESULT 7
US-08-810-009-12
Sequence 12, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0
FILING DATE: 08-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: y1 1.8689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                             DSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSN 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRAFLNVCRHRGKTLVSVEAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGES 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IHQEPERIRQASGVNDLTTQTAASWYVAMRSDALRGKP---VAIKLFGQPLVAWRDGGGR 61
                                                                                                                                                                                                                                                         HMLLAIKKG--DGVVRSAANFILYGLQTWAAAGYDVAIWNSMKAD
                                                                                                                                                                                                                                                                                                   WTYAIVEKDMPEDLKRRLADSV---QRTGGPAGF----WESDDNDNMETASQNGKKYQSR 379
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08-JUN-1994
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Briggs, Steven P.

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US-08-810-009-14
                                                                                                                                                                                                                                                                                                                                                                Patent No. 6211437
GENERAL INFORMATION:
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Best Local Similarity 52.9%;
Matches 18; Conservative
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLIANCE
FILING DATE: 04-MAR. 17.
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
NAME: 32,943
                                                                                                                                                                                                                                                   APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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LENGTH: 35 amino acids
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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APPLICANT: Gray, John
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TELEFAX: 575102
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CITY: Charlotte
STATE: No. 6211437th Carolina
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STREET: P.U. --
CITY: Charlotte
---me. No. 6211437th Carolina
 APPLICATION NUMBER:
                                                                                                                            ZIP: 28234
                                                                                                                                               COUNTRY:
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04-MAR-1997
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US/08/810,009
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Pred. No. 0.00054;
                                      Version
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US-08-810-009-13
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US-08-810-009-13
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Patent No. 6211437
GENERAL INFORMATION:
Query Match
Best Local Similarity
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                                                                                                                                             TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08,
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,94
                                                                                                                                                                                                  TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
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TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: CELL DEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                    MOLECULE TYPE:
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Local Similarity 52.9%;
les 18; Conservative
                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                  TOPOLOGY:
                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                   LENGTH:
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                                                                                                                   amino acid
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                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
4.5%;
52.9%;
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                                                                                                                                                                                                                                                                                                                                                        US/08/810,009
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Score 108; DB 4; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
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               Length 35;
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RESULT 11
US-09-311-626B-4
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                                                                                                                    GENERAL INFORMATION:
                                                                                                                                    Sequence 4, Application US/09311626E Patent No. 6399347
                                           APPLICANT:
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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       APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
                                                                          APPLICANT:
                                                                                   APPLICANT: Jorgensen, Per
APPLICANT: Schnorr, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 04-MAR-19'
CLASSIFICATION: 800
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APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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APPLICATION NUMBER: US/09/311,626B
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5. 6211437
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                                                      Andersen, Lene No. 6399347boe Schulein, Martin
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                                                                                                                                                                                                                                                                                                 4.5%;
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                                                                                                                                                                                                                                                                                             Score 108; DB 4;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                   Mismatches
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                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION MIMBER: US (08 /810 009
                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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RESULT 12
US-08-810-009-9
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                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08810009 Patent No. 6211437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: 60/084,
PRIOR FILING DATE: 1998-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 622
TYPE: PRT
ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                   APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.'
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLAN
                                                                                                                                                                   NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
STREET: P.U. STREET: P.U. STREET: P.U. STREET: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 WREEVVWRAEDSSELRIYTTIDVTEHRMYTLMHDAVYRLGIAWQNVGYNQPPHTGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 WGVHAGKDVGRGMAADIDPRYEGAEVWANGSLYTAKGV-KIGNTLPSSTNFGIW----- 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 -----NKEIG-DVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTT-EVWTYAIVE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 SIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERL- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 YLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 NRVDRFLAGVAYLDGERPSFVMARGYYTRTVLVAYNFRG----GKLTKLWTFDSDAPGNGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 KGKVIGNANADYRNAQGRILSGPEYLTVFKG---DTGAELTTVNYEPARGNVADWGDSYG 301
                                                                                                 ADDRESSEE: BELL, SELL, STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 RGKTLVSVEAG--NAKGFVCS-----YHGWGFGSNGELQSVPFEK------DLYG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 21.6 es 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAGQG-----NHSLSVADVDGDGKDEIIYGAMAVDHDGKG-LYSTGWGHGDAMHTGN 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESLNKKCLGL-----CFDQEAPPLMD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VHENSNSPYGLSFRDAKTGKII 443
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21.6%;
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                                                                                                                                            PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 4; Length 622; Pred. No. 0.072;
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APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997

#1.30

CLASSIFICATION:

PRIOR APPLICATION DATA:

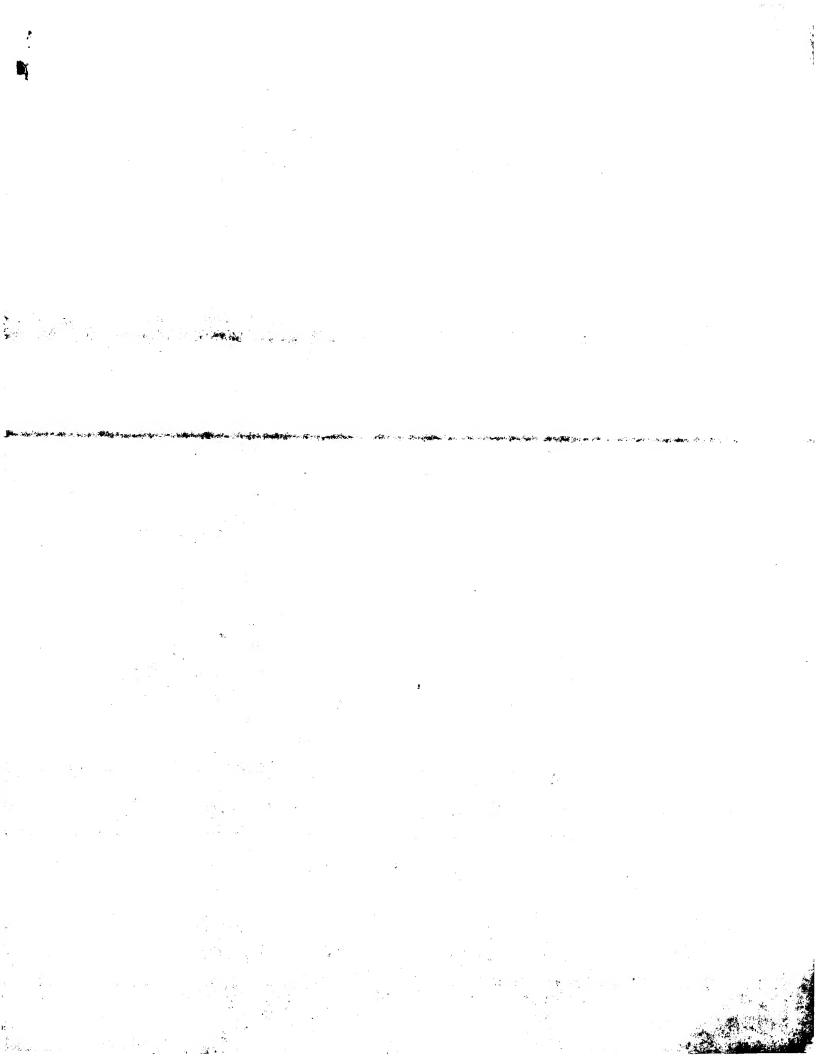
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                                                                                                                                                          SOFTWARE: Patentin Release #10, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/809,326A
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION UMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION UMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. blussing Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                             FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
COUNTRY:
                                                                                                           APPLICATION NUMBER: FILING DATE: 28-API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ட
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQCRHRGMRICRSDAGNAKAPTCSYHGWAYDIAGK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Pennie & Edmonds LLP
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obara, Kazuhiko
Matsumoto, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Izutsu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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28-APR-1995
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51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, NAS CODING FUSED PROTEINS CONTAINING THE POLYPEPTIDES, NAS CODING THEREFOR, RECOMBINANT VECTORS CARRYING THE DAS, TRANSFORMANTS CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA PREUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA PREUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA PREUMONIAE GENE, AND METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA PREUMONIAE GENE
                                                                                                                                              JP 106008/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
                              JP 106009/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32,943
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Pred. No. 0.0013;
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RESULT 14
US-08-809-326A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08809326A
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                                                                                                                                                                       APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLAMYDIA
TITLE OF INVENTION: CUSED PRO'
TITLE OF INVENTION: CONTALININ
TITLE OF INVENTION: CONTALININ
TITLE OF INVENTION: ANTIBODY,
TITLE OF INVENTION: PNEUMONIAI
TITLE OF INVENTION: MEASUREMET
TITLE OF INVENTION: REAGRATS!
TITLE OF INVENTION: PNEUMONIAI
TITLE OF INVENTION: PNEUMONIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-9090
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 KSAIGETS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 KDKTSSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 AGFWESDDNDNME----TASQNGKKYQSRDSD-----LLSNLGFGEDVYGDAVYPGVVG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 V----FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 WKAPAENFVGDAYHVGWTHASSL-----RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 GSGMGVLWDGYSGVHSADL------VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
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TELEFAX: (¿1,
TELEX: 66141 PENNIE
                                                                                     STREET:
                      COUNTRY:
                                                STATE:
                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GTDDRVTW-----VKSVDEAIAACGDVPEIMVIGGG---RVYEQFLPKAQKLYLTHIDAE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 WNLPAD------KNIILSSQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 21.4 nes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 1 FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAGASG
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10036-2711
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                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller, Charles E.
                                         New York
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                                                                                     1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                      Obara, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                           Izutsu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                              Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hiroshi
                                                                                                                                                                                                            CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, DNAS CODING
FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4%; Score 105.5; DB 21.4%; Pred. No. 0.072;
                                                                                                                                                                            PNEUMONIAE GENE
                                                                                                                                                                                                   REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP 106011/95
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RESULT 15
US-08-810-009-18
: Sequence 18, Application US/08810009
: Patent No. 6211437
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Best Local Similarity 21.4
Matches 53; Conservative
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elling CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 224711/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 10
FILING DATE: 28-APR-1995
ATTORNEY_AGENT INFORMATION:
NAME: Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 10 FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: JP 106008/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 74:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             300 V-----FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGP 354
                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                      247
                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 WKAPAENFVGDAYHVGWTHASSL-----RSGESIFSSLAGNAALPPEGAGLOMTSKY 246
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                                                                                                                                                                                                                                                                                                                                                                                                                      22 WNLPAD------LAWFKRNTLNKPVIMGRHTWESIGRPLPGR------KNIILSSQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 10 FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                             KDKTSSTT 232
                                                                                                                                                               KSAIGETS 412
                                                                                                                                                                                                 -----DNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAGASG 224
                                                                                                                                                                                                                                      AGFWESDDNDNME----TASQNGKKYQSRDSD-----LLSNLGFGEDVYGDAVYPGVVG
                                                                                                                                                                                                                                                                        VEGDTHFPDYEPDDWESVFSEFHDADAQNSHSYEFEILE-----RRILMSISSSSGP 170
                                                                                                                                                                                                                                                                                                                                              GTDDRVTW-----VKSVDEAIAACGDVPEIMVIGGG----RVYEQFLPKAQKLYLTHIDAE 118
                                                                                                                                                                                                                                                                                                                                                                                GSGMGVLWDGYSGVHSADL------VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
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19-MAR-1997
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21.4%; Pred. No. 0.14;
ative 38; Mismatches
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Search completed: January 27, 2003, 09:04:53 Job time: 11.1667 secs
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                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-810-009-18
                                                                                                                                                                          Query Match
                                                                                                                                         Matches
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TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SPEUII, W. MUITAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919.881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 919-00-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: NO. 6211437th Carolina
                                                                                                                                         Local Similarity nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                     1 NSCRHRGALLCPFSKGNQKFHVCRYHGWSYDSSG
                                                                                                                                                                                                                                                                               amino acid
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Johal, Gurmukh S.
Gray, John
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-1997
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                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                          5718-4
                                                                                                                                                          Score 104; DB 4;
Pred. No. 0.0021;
                                                                                                                                         Mismatches
                                                                     34
                                                                                                                                                                        DB 4; Length 35;
                                                                                                                                         Indels
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Title:
Perfect score:
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                                                                                                                                                                 OM protein - protein search, using sw model
                     US-09-843-250-32
2410
                                                                            January 27, 2003, 08:54:32; Search time 25.8333 Seconds (without alignments) 3581.232 Million cell updates/sec
MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                               GenCore version 5.1.3 Compugen Ltd.
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_bacteria
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organell:
9: sp_phage:*
10: sp_plant:*
11: sp_vicus:*
12: sp_virus:*
13: sp_vertebr
13: sp_vertebr
14: sp_unclass
15: sp_bacteri
16: sp_bacteri
17: sp_archeap sp_archea:*
sp_bacteria:* sp_invertebrate:*
sp_mammal:* sp_organelle:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

sp_rodent:*
sp_virus:*

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	o	U	4	ω	۵	1	No.	Result	
1405	1451	1483	1484	1486	1488	1490	1966.5	2019	2048	2068	2186	2190	2205	2289	2329	Score		
58.3	60.2	61.5	61.6	61.7	61.7	61.8	81.6	83.8	85.0	85.8	90.7	90.9	91.5	95.0	96.6	Match	Query	ф
277	277	277	277	277	277	277	451	447	447	447	447	447	449	449	449	Match Length		
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Q9EUC7	Q9F5S3	Q9F5S9	Q9F5S8	Q9F5T3	Q9F5S4	Q9ETK2	Q45695	Q8RTL4	P95564	Q8VUD4	052382	Q9L5D2	Q9ZI73	Q52142	Q938R9	ID		
Q9euc7 pseudomonas	Q9f5s3 pseudomonas	Q9f5s9 pseudomonas	Q9f5s8 pseudomonas	Q9f5t3 pseudomonas	Q9f5s4 pseudomonas	Q9etk2 pseudomonas	Q45695 burkholderi	Q8rtl4 comamonas s	P95564 pseudomonas	Q8vud4 burkholder:	O52382 ralstonia	Q915d2 comamonas	Q9zi73 pseudomonas	Q52142 pseudomonas	Q938r9 pseudomonas	Description		

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
1002	1009	1016	1038	1038	1039	1040	1042.5	1067	1110.5	1123	1127	1134	1134	1139	1352.5	(4)	ta	1393	1393	1393	1393	1393	1396	1396	1399	1399	1402	1403	\
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Q93M41	Q93M39	Q93M40	Q8VUM2	Q8VR21	Q8VUM5	Q9F6B6	Q9WXG8	Q8VR25	Q93NA8	Q8VR22	Q8VR24	Q8VL21	Q8VR23	Q8VUM6	Q92HH3	Q9F5S2	Q9F5T7	Q9F5S6	Q9F5T0	Q9F5T1	Q9F5T2	Q9F5T4	Q9F5S7	Q9F5T6	Q9F5S5	10	Q9F5T5	Q9F5T8	
Q93m41 uncultured	9	0	Q8vum2 ralstonia s		Q8vum5 napthalene	Q9f6b6 marinobacte	Q9wxg8 alcaligenes	Ģ	Φ.	N	4	μ.	Q8vr23 pseudomonas		~	582	_	Q9f5s6 pseudomonas			N		Q9f5s7 pseudomonas			etv3	f5t5	Q9f5t8 pseudomonas	

ALIGNMENTS

Qy	Qy Db	Оу	7 H.O	SQ	DR	DR DR	DR	DR.	Z R	RA	RP	RN	200	88	SO	GN	DE	D I		AC	ID	RES Q9
QY 121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL	Qy 61 IDEVIVSRONDGSTRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELOSVÞFE 	QY 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 	Query Match 96.6%; Score 2329; DB 2; Length 449; Best Local Similarity 96.0%; Pred. No. 4e-171; Matches 431; Conservative 12; Mismatches 6; Indels 0;	SQ SEQUENCE 449 AA; 49608 MW; 5EFEDBE0282FE812 CRC64;	PROSI		InterPro;	DR InterPro; IPR001281; Rieske.	Submitted (OCT-2001) to the	Min KH., Ji SH.;		RN [1]			OS Pseudomonas fluorescens.	NAHAC.	Naphthalene dioxygenase.	01-DEC-2001 (ILEMBLIEL. 01-MAR-2002 (TrEMBLIEL.	01-DEC-2001 (TrEMBLrel. 19,	Q938R9;	ID Q938R9 PRELIMINARY; PRT; 449 AA.	RESULT 1 Q938R9
180	120 120	60	Gaps																			

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RESULT
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Query Match
Best Local Similarity
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Yue-Wu W., Masao I
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Q52142; O08194;
Q1-NOV-1996 (Tre
Q1-NOV-1996 (Tre
Q1-DEC-2001 (Tre
                    InterPro: IPR001281; Rieske.
InterPro: IPR001663; Ring_hydroxyl_A.
InterPro: IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
                                                                                                     Submitted (JUN-1997) to the EMBL; AB004059; BAA20391.1; HSSP; P23094; INDO.
                                                                                                                                               chromosomes
                                                                                                                                                                                                                    "Identification and characterization of genes encoding polycyclic aromatic hydrocarbon dioxygenase and polycyclic aromatic hydrocarbon dioxygenase and polycyclic aromatic hydrocarbon dihydrodiol dehydrogenase in Pseudomonas putida OUS82."; J. Bacteriol. 176:2444-2449(1994).
                                                                                                                                                                                       STRAIN-OUS82;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-OUS82;
                                                                                                                                                                                                                                                                                                                                  STRAIN-OUS82;
Takizawa N.;
                                                                                                                                                                                                                                                                      MEDLINE-94209249; PubMed-8157615; TAKIZAWA N., Kaida N., Torigoe S.,
                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                             <iyohara H.;</pre>
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                                                                                                                                                                   Toshiya I.,
Masao F., H
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of Pseudomonas
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2289; DB 2;
No. 4.8e-168;
                                                                                                                                                                           Kazuhiro
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                                                                                                                                                                       Gene 236:149-157(1999).
EMBL; AF039533; AAD02136.1; -.
HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1
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Q9ZI73;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic characterization and evolutionary implications of chromosomally encoded naphthalene-degradation upper pathwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAHAC
                                                                                                                                  Dioxygenase
SEQUENCE '
                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas stutzeri AN10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bosch R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=316;
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                                                                 Similarity
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1 (TrEMBLrel. 19, La
2 dioxygenase Fe-S
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89.5%;
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S large subunit.
                                       Score 2205; D
Pred. No. 1.4e
25; Mismatches
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Best Local :
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                Appl. Microbiol. Biotechnol. 55:609-6
EMBL; AF25250; AAF72976.1; -.
HSSP; P23094; 1ND0.
Interpro; IPR001281; Rieske.
Interpro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                       Dioxygenase
                                                                                                                                                                                                                                                                                                      pfam; pF00355; Rieske; 1.

pfam; pF00848; Ring_hydroxyl_A; 1.

pRINTS; pR00090; RRDDIOXGNASE.

PROSITE; pS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Insights into the genetic diversity of initial dioxygenases degrading bacteria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
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                      IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                  MIYEN--LVSEAGLTQKHLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVTAKMG
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                                                                                                                                                                                                                                                               49548 MW;
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                                                                                                                                                                                         Score 2190;
Pred. No. 2
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                                                                                                                                                                                                                                                               2950EF36123A6F21 CRC64;
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  Matches
             Query Match
Best Local (
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01-JUN-1998
01-JUN-1998
01-DEC-2001
                                                                Interpro; IPR001281; Rieske.
Interpro; IPR001563; Ring_hydroxyl_A.
pfam; PF00355; Rieske; 1.
pfam; PF00848; Ring_hydroxyl_A; 1.
pRINTS; PR00090; RNGDIOXGNASE.
pROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                     Zhou N.Y., Fuenmayor S.L., Williams P.A.;
"nag genes of ralstonia (Formerly pseudomonas)
enzymes for gentisate catabolism.";
J. Bacteriol. 18:700-708(2001).
EMBL; AF036940; AAD12610.1; -.
HSSP; P23094; INDO.
                                                                                                                                                                                                                                                    "Ruenmayor S.L., Wild M., Boyes A.L., Williams
"A gene cluster encoding steps in conversion
gentisate in Pseudomonas sp. strain U2.";
J. Bacteriol. 180:2522-2530(1998).
                                               SEQUENCE
                                                          Dioxygenase;
                                                                                                                                                                                                          MEDLINE-20576173;
                                                                                                                                                                                                                      STRAIN=U2
                                                                                                                                                                                                                                                                                                                STRAIN=U2
                                                                                                                                                                                                                                                                                                                                                            Ralstonia
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pWWU2
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   MEDLINE=98233751; PubMed=9573207;
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=70356;
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             Similarity
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  Conservative
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                                                          Plasmid.
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                                              AA;
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                                              49570 MW;
             90.7%;
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Last annotation updat
large oxygenase compo
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           Score 2186;
Pred. No. 4
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              Query Match
Best Local Similarity
Matches 375; Conser
                                                           Johnson G.R., Jain R.K., Spain J.C.;

"Origins of the 2,4-dinitrotoluene pathway.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF169302; AAL50021.1; -.

InterPro; IPR001281; Rieske.

InterPro; IPR001663; Rieske.

InterPro; IPR001665; Rieske; 1.

Pfam; PF00355; Rieske; 1.

Pfam; PF00348; Ring_hydroxyl_A; 1.

PFAm; PF00848; Ring_hydroxyl_A; 1.

PFAM; PF00090; RING_HYDNOXYL_ALPHA; UNKNOWN_1.

R PROSITE; PR00090; RING_HYDNOXYL_ALPHA; UNKNOWN_1.

SEQUENCE 447 AA; 49468 MW; 2A5BF8558320275C CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Q8VUD4;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                 MEDLINE=20254695; PubMed=10795678; Johnson G.R., Jain R.K., Spain J.C.; Topperties of the trihydroxytoluene oxygenase from Burkholderia cepacia R34: an extradiol dioxygenase from the 2,4-dinitrotoluene pathway.";
                                                                                                                                                                                                                                                                                                                                           Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VUD4
                                                                                                                                                                                                                     Arch.
                                                                                                                                                                                       STRAIN-R34
                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                   Burkholderia
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                     Conservative
                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
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                                85.8%;
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                     38;
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Last sequence up
                   Score 2068; DB 2;
Pred. No. 5e-151;
8; Mismatches 34;
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                                         Length
                     Indels
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                                                                                                                                                                                 Query Match
Best Local Sin
Matches 376;
                                                                                                                                                                                                                                                                                                                   EMBL; U4504; AAB40383.1; -.
HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00099; RNGDIOXGNASE.
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P95564;
01-MAY-1997
01-MAY-1997
01-JUN-2001
                                                                                                                                                                                                                                                                            PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parales J.V., Kumar A., Parales R.E., Gibson I "Cloning and sequencing of the genes encoding allowances from Pseudomonas sp. JS42.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dioxygenase from Pseudomonas
Gene 181:57-61(1996).
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Bacteria; Proteobacteria
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                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                            PS00570; RING_HYDROXYL_ALPHA; 1.
447 AA; 49485 MW; 1CB0E223E528E3BD CRC64;
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(TrEMBLrel.)
                                                                                                                                                                                    Conservative
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83.7%;
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03,
17,
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                                                                                                                                                                                 Score 2048; D:
Pred. No. 1.7e
34; Mismatches
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Last sequence update)
Last annotation update)
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Best Local S
Matches 368
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                       MEDLINE=21681044; PubMed=11823201;
Lessner D.J., Johnson G.R., Parales R.E., Spain J.C.,
"Molecular Characterization and Substrate Specificity
Dioxygenase from Comamonas sp. Strain JS765.";
Appl. Environ. Microbiol. 68:634-641(2002).
EMBL; AF379638; ARJ/6202.1; -
SEQUENCE 447 AA; 49556 MW; 4CA961F99A37DF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8RTL4
                                                                                                                                                                                                                                                                                                                                                                                                          Oxygenase-alpha
                                                                                                                                                                                                                                                                                                                                  STRAIN-JS765;
                                                                                                                                                                                                                                                                                                                                                                                    Comamonas sp.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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239
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           QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                   ELYGPPGKVVIKANWKAPAENFYGDAYHYGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                         IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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                                       ELVGPPGKVVVKANWKSFAENFVGDGYHVGWTHAAALRAGQSVFSSIAGNAKLPPEGAGL
                                                                                                                           VDEVIVSRQNDGSVRAFLNVCRHRGKTLVHAEAGNAKGFVCGYHGWGYGSNGELQSVPFE
                                                                                                                                                                     MSYQN--LVSEAGLTQKLLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVKAKMG
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                                                                                                                                                                                                                368;
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
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? (TrEMBLrel.
? (TrEMBLrel.)
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82.0%;
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Last annotation updat
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Pred. No. 3e
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of Nitrobenzene
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Best Local S
Matches 359
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EMBL: U62430; AAB09766.1; -.
HSSP: P23094: INDO.
InterPro: IPR001281; Rieske.
InterPro: IPR00163; Ring_hydroxyl_A.
Pfam: PF00355; Rieske; 1.
Pfam: PF00848; Ring_hydroxyl_A; 1.
PRINTS: PR00090; RNGDIOXGNASE.
PRINTS: PR00090; RNGDIOXGNASE.
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity to naphthalene dloxygenase."; J. Bacteriol. 178:4926-4934(1996).
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Q45695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suen W.C., Haigler B.E., Spain J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96326338; PubMed=8759857,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia sp.
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 361
                       304
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                                 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                  QATTKYGSGIGVSLDAYSGVQSADLVPEMMAFGGAKQEKLAKEIGDVRARIYRSQVNGTV
                                                                             QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                         ELYGPPGKVVIKANWKAPAENFYGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                         VDEVIVSRQNDGSVRAFLNVCRHRGKTIVDAEAGNAKGFVCGYHGWGYGSNGELQSVPFE
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                      FPNNCFLTGAGVFKVFNPIDENTTEAWTYAIVEKDMPEDLKRRLADAAQRSTGPAGYWES
                                                                                                              ELYGPPAKYVYKGNWKYFAENFYGDIYHIGWTHASILRAGQAIFAPLAGNAMLPPEGTGL
                                                                                                                                                                                                                  IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                         PS00570; RING_HYDROXYL_ALPHA; 1.
451 AA; 49827 MW; 726796C29CEF9A10 CRC64;
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                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                41;
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Last sequence up
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l; Mismatches
                                                                                                                                                                                                                                                                                                                    Score 1966.5;
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Q9ETK2
ID Q9ETK2
AC Q9ETK2
DT Q1-MAR-
DT Q1-MAR-
DT Q1-DEC-
DE Naphtha
GN NAHAC2
OS Pseudom
OC Bacter1
OC Pseudom
OC Pseudom
CN NCBI_Ta
RN [1]
RP SEOUENC
RT "COEX1S
RT PSEUDOM
RT PSEUDOM
RT PSEUDOM
RT SEOMBL: A
DR EMBL: A
DR EMBL: A
DR HSSE; P
DR INTERP
DR INTERP
DR FIRMTS;
DR Pfam; P
DR Pfam; P
DR PROSITE
KW NON_TER
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SQUENC
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Best Local Similarity
Matches 277; Conserv
  Q9F5S4;
Q9F5S4;
01-MAR-2001
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01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                          Dioxygenase.
NON_TER
NON_TER 2
                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001281; Rieske.
Interpro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00488; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=2IDINH, PRIMN1, AND 3IA2NH; Ferrero M.A., Lalucat J., Bosch R.; Ferrero M.A., Lalucat J., Bosch R.; "Coexistence of two naphthalene dioxygenase genes (nahAc) Pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
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                                                                                 LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 332
                                                                                                                                                                                                                                     SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                                                                                                                                                                                                 TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ 115
                                                                                                                              EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH
                                                                                                                                          EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH
                                                                                                                                                                            HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
                                                                                                                                                                                       HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
                                                                                                                                                                                                                         SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK
                                                                                                                                                                                                                                                                     TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF306438; AAG25698.1; -. AF306432; AAG25692.1; -. AF306436; AAG25696.1; -. P23094; INDO.
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277
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ilarity 100.0%;
Conservative
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  (TrEMBLrel.
                          PRELIMINARY;
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277
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. 16, Last sequ
. 19, Last anno
e iron sulfur |
  16,
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  Created)
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Pred. No. 8.2e-107;
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Last annotation update)
sulfur protein 2 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                               BFCF9B5A379546DB CRC64;
                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                    295
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RESULT 12
Q9F5T3
ID Q9F5T3
AC Q9F5T1
AC Q9F5T1
DT 01-MA
DT 01-DE
Napht
GN NAHAC
OS Pseud
OC Bacte
OC Pseud
OX NCBL,
RN [1]
RP SEQUE
RC STRAI
RA FETTE
RA FETTE
RA PSEUD
RI OSS
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HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00848; Ring_hydroxyl_A; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                    Q9F5T3;
Q9F5T3;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dioxygenase.
NON_TER
NON_TER
2
                                                                                            Pseudomonas
                                                                                                      Bacteria; Proteobacteria;
                                                                                                                   Pseudomonas
                                                                                                                                       Naphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2000) to the EMBL; AF306440; AAG25700.1;
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                                              STRAIN=19IIDNH;
                                                         SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=139738
                                                                                                                                NAHAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=303;
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277 AA;
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99.6%;
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Last annotation updat
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Ferrero M.A., Lalucat J., Bosch R.; "Coexistence of two naphthalene dioxygenase genes Pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ data
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PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrero M.A., Lalucat J., Bosch R.; "Coexistence of two naphthalene dioxygenase genes Pseudomonas strains from West Mediterranean Sea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAKMGIDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                  LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV
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16, Last sequence update)
19, Last annotation update)
iron sulfur protein (Fragment).
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Pred. No. 1.
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                                                                                                                                                                     subdivision;
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2 (Fragment).
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Query Match
Best Local Similarity
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Best Local :
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Q9F5S8;
Q1-MAR-2001
Q1-MAR-2001
Q1-DEC-2001
                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                      Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase ge
Pseudomonas strains from West Mediterranean Se
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AF306434; AAG25694.1; -
HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas sp. razza....
Psanteria; Proteobacteria;
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PR3MN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Naphthalene
                                                                                                                           Dioxygenase
                                                                                                                                                 PROSITE;
                                                                                                                                                                   PRINTS; PR00090; RNGDIOXGNASE
                                                                                                                                                                                                                        InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=139773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ 115
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                                                                                                                                                                                       PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
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                                                                                                                                               PS00570; RING_HYDROXYL_ALPHA;
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277
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277 AA;
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30064 MW;
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61.6%;
99.6%;
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16, Last sequence update)
19, Last annotation update)
19 iron sulfur protein (Fragment).
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Pred. No. 1.
Score 1484;
Pred. No. 2
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2.4e-106;
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.7e-106;
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Sea. ";
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Matches 276;
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NON_TER
NON_TER
SEQUENCE 27
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Q9F5S9;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                      Pseudomonas strains from West Mediterranean Se Submitted (SEP-2000) to the EMBL/GenBank/DDBJ EMBL; AF306433; AAG25693.1; -. HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                              InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Naphthalene
                                                                                                                                                                                                                                                     PROSITE; PS00570;
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                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=8IDINH;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAHAC
 236
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                     TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ
                                                                             SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                               TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV
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EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH
                                                                   SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK
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                                                                                                                                                                      Similarity
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277 AA;
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l (TrEMBLrel. 16,
l (TrEMBLrel. 19,
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99.6%;
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Last annotation updat
n sulfur protein (Frag
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Pred. No. 2.8e
0; Mismatches
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editerranean Sea.";
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Search completed: January 27, Job time: 27.8333 secs
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Best Local Similarity
Matches 268; Conserva
                                                                                                                                                                                                                                                                                                                                            Dioxygenase.
NON_TER
NON_TER
SEQUENCE 27
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"Coexistence of two naphthalene dioxygenase genes (nahAc)
"Seudomonas strains from West Mediterranean Sea.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF306441; AAG25701.1;
HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
pfam; PF00355; Rieske; 1.
pfam; PF00848; Ring_hydroxyl_A; 1.
pfam; PF00848; Ring_hydroxyl_A; 1.
pRINTS; PR00099; RNGDIOXGNASE.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein 1 (Fragment).
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                                               LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 332
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            2003,
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GenCore version 5.1.3 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 27, 2003, 08:47:32; Search time 7.16667 Seconds (without alignments) 2598.540 Million cell updates/sec

Title: Perfect score:

Sequence: US-09-843-250-32
2410
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 3 3 3 3 3 3 3	Result No.
2401 2315 2316 47.5 6447.5 614.5 614.5 614.5 614.5 614.5 614.5 614.5 614.5 614.5 614.5 284.5 239.5 239.5 239.5 239.5 111	Score
11122222222222222222222222222222222222	Query Match L
31	Length DB
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ALIGNMENTS

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SEQUENCE FROM N.A. SPECIES-P.Dutida; STRAIN-BS202; PLASMID-NPLI; SPECIES-P.Dutida; STRAIN-BS202; PLASMID-NPLI; Bezborodnikov S.G., Boronin A.M., Tiedje J.M.; "Nucleotide sequences of genes encoding an upper pathway of naphthalene metabolism of NPLI plasmid from Pseudomonas putida strain BS202."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. [6]	·· ct fb C L Cu Ft	FROM N.A. P.putida; S P.putida; S J.V., Paral d (MAR-1996 FROM N.A. 18; 18; 94042852; P 94042852; P -A., Stanle ism of dibe complete D m;	rsequomonas. NCBL_TaxID=303, 306; [1] SEQUENCE FROM N.A. SPECIES-P.putida; STRAIN=NCIB 9816; SPECIES-P.putida; STRAIN=NCIB 9816; MEDLINE-89211973; PubMed=3243438; MEDLINE-89211973; Pub	

0,

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EMBL; M23914; AAB47591.1; -.
EMBL; U49496; AAA92111.1; -.
EMBL; M60405; AAA16125.1; -.
EMBL; M83949; AAA25902.1; -.
EMBL; AF001471; AAB62707.1; -.
EMBL; AF0004284; AAB61373.1; -.
EMBL; AF0004284; AAB61373.1; -.
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VARIANT
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InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PP00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00099; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAPHTHALENE DIHYDRODIOL.

NAPHTHALENE DIHYDRODIOL.

CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,25)-1,2-

CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,25)-1,2-

CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,25)-1,2-

COLVERSION OF PROBABLY BINDS A 2FE-2S GROUP AND IRON ATOM.

PARTHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERTS PHENANTHRENE: CONVERTS PHENANTHRENE - CONVERTS PHENANTHRENE - CONVERTS PHENANTHRENE - LAWRENCH - CONVERTS PHENANTHRENE - CONVERTS PHENANTHRENE - LAWRENCH - COMPONENT ENZYME SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN (NDOA), AND 1SP I. COMPOSED OF AN HEXAMER OF THREE LARGE ALPHA SUBUNITS (NDOB) AND THREE SMALL BETA SUBUNITS (NDOC) - SIMLLARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                   Dioxygenase;
METAL
                                                                                                                                                                                                                                                                                                                                                             Aromatic hydrocarbons catabolism; Oxidoreductase;
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MEDLINE=98298434;
                                                                          VARIANT
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Ramaswamy S.;
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X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
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MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION OF
BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
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PubMed=9634695;
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15-DEC-1998
15-JUN-2002
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                                                          Hamann C.;
Submitted (JUN-1997)
                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 17483;
                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Naphthalene 1,2-dioxygenase alpha subunit (EC
1,2-dioxygenase ISP alpha).
                                                                                                                    NCBI_TaxID=294;
                                                                                                                                            Bacteria;
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                      mitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: COMPONENT OF NAPHTHALENE DIOXYCENASE (NDO)
MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION
BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CIS-
             NAPHTHALENE DIHYDRODIOL
                                                                                                                                                                                 OR NDOC2
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C -> R (IN STRAIN G7).

H -> D (IN STRAIN G7).

1FD2F42296B4F7A8 CRC64;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT AND AN IRON SULFUR PROTEIN (15P). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS COMPOSED OF A LARGE ALPHA SUBUNIT (NDOB) AND A SMALL BETA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydronaphthalene-1,2-diol + NAD(+).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES

CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF

DIBENZOTHIOPHENE (DET) AND PHENANTHRENE. CONVERTS PHENANTHRENE

1-HYDROXY-2-WAPTHOLC ACID AND THE METABOLISM OF DET IS LIMITED

OXIDATION OF THE AROMATIC RING.
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PR00090; RNGDIOXGNASE.
; PS00570; RING_HYDROXYL_ALPHA;
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IRON (BY SIMILARITY).
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2e-173;
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                        Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                       EMBL, D84146; BAA12240.1; -.
HSSP: P23994; 1NDO.
InterPro; IPR001261; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                    Aromatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas
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SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
DIOXYGENASE ALPHA SUBUNIT FAMILY.
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                                                                   hydrocarbons
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                                                                                                                                                             STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                   Turlin E., Gasser F., Submitted (SEP-1994)
SEQUENCE
                                        "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                   Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                          SEQUENCE FROM N.A
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, Goeden M.A., Rose I
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RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
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RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
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RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Sasawara N., Yasuara N., Yasuar
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                       FERREDOXIN (HCAC) AND A FERREDOXIN REDUCTASE (HCAD). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
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MBL outstation way

EMBL; 237966; CAA86018.1; -. EMBL; AE000340; AAC75591.1; -. EMBL; AE000883; BAA16433.1; -. EMBL; AE00884; BAA1643.1; -. EMBL; AE005484; AAG57651.1; -. EMBL; AE002562; BAB36827.1; -. EMBL; AP002562; BAB36827.1; -. HSSP; P23094; INDO. ECOGENE; EG13456; hcaE. Dioxygenase; METAL METAL METAL 1 pfam; pF00355; Rieske; 1.

pfam; pF00848; Ring_hydroxyl_A; 1.

pfam; pF00890; RNGDIOXGNASE.

PRONITS; pR00090; RING_HYDROXYL_ALPHA; 1. InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A. Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; 85 87 105 Complete 85 87 105 proteome. IRON-SULFUR IRON-SULFUR IRON-SULFUR (2FE-2S) (2FE-2S) (2FE-2S) Iron-sulfur; Iron; (BY (BY) Y SIMILARITY).
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01-NOV-1995 (Rel. 32, Created)

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Benzene 1,2-dioxygenase alpha
                                                dioxygenase are unusual in codon usage Gene 130:33-39(1993).
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Tan H.-M., Tang H.-Y., Joannou C., Abdel-Wahab N.H.,
"The Pseudomonas putida ML2 plasmid-encoded genes fo
                                                                                                            STRAIN=ML2;
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CATALYTIC ACTIVITY: Benzene + NADH dihydrobenzene-1,2-diol + NAD(+).
COFACTOR: PROBABLY BINDS A 2FE-2S (
PATHWAY: FIRST STEP OF DEGRADATION
                                                                                                                                                                                                                                                                                                                                  ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
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PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                   KMMTSPDW
                                                                                                             AHVSSSNW
                                                                                                                                                                DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ 421
                                                                                                                                                                                                                                                WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF
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                                                                                                                                                                                                                                                                                                      WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP-----KFGKQYRAS
                                                                                                                                                                                                                                                                                                                     WKAPAENFYGDAYHYGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
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                                                                                                                                      DGENWVEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
                                                                                                                                                                                           PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
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IPR001663; Ring_hydroxyl_A.
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                                                                                   443
                                                                                                             429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
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IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON (BY SIMILARITY) .
IRON (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 649.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1ECD5EA6C4CF72C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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(BY SIMILARITY).
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TOD1_PSEPU P13450;

STANDARD;

PRT;

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Best Local S
Matches 145
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01-JAN-1990
15-JUN-2002
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or send a
                                                                                                                                                                                                                                                                                                                 METAL
METAL
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00090; RNGDIOXGNASE PROSITE; PS00570; RING_HYDROX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                 Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00570; RING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A36516; A36516.
HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04996; AAA26005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Toluene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zylstra G.J., Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89359301; PubMed-2670929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas
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                                                      195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. PATHWAY: Toluene degradation; first step. SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (TODC1 AND FERREDOXIN (TODB) AND A FERREDOXIN REDUCTASE (TODA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   todC1C2BADE genes
VLWDGYSGVHSADLVPELMAF---GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                         WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                                   WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                             PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                                     --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                               QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                               VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE---
                                                                                                                                                                                                           IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                 IYTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLN
                                                                                                                                                                                                                                     al Similarity
145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Pro; IPR001663; Ring_hydroxyl_A.
PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1C2BADE genes and their expression Chem. 264:14940-14946(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              degradation by Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02 (Rel. 41, Last annotation update)
,3-dioxygenase alpha subunit (EC 1.14.12.-).
                                                                                                                                                                                                                                                                                        228
450 AA;
                                                                                                                                                                                                                                                                                                              NAD.
96
98
116
119
222
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(Rel. 13,
(Rel. 41,
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BELONGS TO THE BACTERIAL RING-HYDROXYLATING
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116
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228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rieske.
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                             catabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                          _HYDROXYL_ALPHA;
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                                                                                                                                                                                                                                                                                                               IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                 Score 647.5; DB 1
Pred. No. 3.6e-43;
                                                                                                                                                                                                                                                                                        038C80F197F3485D CRC64;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdivision; Pseudomonadaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÇĘ,
                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
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                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                   181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence
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ХВ)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                Haddock J.D., Gibson D.T.;
J. Bacteriol. 178:2158-2158(1996).
J. CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) =
phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron.
                                                                                                                                                                                                                                                                                                                                                  "Purification and Characterization phensing 3.3-dioxygenase from Pseud J. Bacteriol. 177:5834-5839(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erickson B.D., Mondello F.J.;
"Nucleotide sequencing and transcriptional mapping of the encoding biphenyl dioxygenase, a multicomponent polychlorinated biphenyl-degrading enzyme in Pseudomonas s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12.18) (Biphenyl 2,3-
                                       or send
                                                                   modified
                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96011369; PubMed=7592331;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LB400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-LB400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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                                                      entities
                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P37333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 174:2903-2912(1992)
                                                                                             European Bioinformatics Institute
                                                                                                                                                                 SUBUNIT: Heterohexamer consisting of three BphA sububphE subunits. A ferredoxin (BphE) and a ferredoxin (BphG) must be present to obtain activity.

SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLAT
                                                                                                                                                     DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                    PATHWAY: Biphenyl-polychlorinated
                                                                                          SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                  γģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D₩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
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                                         an email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443
                                       requires a license agreement (san email to license@isb-sib.ch).
                                                                 non-profit institutions as long as and this statement is not removed. U
                                                                                                                                                                                                                          step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Pseudomonas cepacia). eria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                 from Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                  activity.
RIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458
                                                                                                                                                                                                                                      and 1 iron atom per subunit biphenyl degradation pathwa
                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA
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                                                                                                                                                                                                                                                                                                                                                                 oxygenase component of sp. strain LB400.";
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                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas strain
                                                                               its content
                                                                                                                                                                                                           subunits and three
                                                                                             restrictions on
                                                                   and
                                                                                                                                                                                              reductase
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                                                                                                                                                                                                                                      pathway;
                                                                   for
                                                                                                             collaboration -
                                                                                                            outstation
                                                                                  nī
                                                                 commercial
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EMBL; M86348; PIR; B41858; F

B41858

AAB63425.1;

HSSP; P23094;

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BPHA_COMTE
ID BPHA_C
AC Q46372
AC Q46372
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUN
DE B1Phan
DE dioxyg
GN BPHA.
OS COmano
OC Bacter
OX NCBI_T
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RA Sylves
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Best Local S
Matches 146
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INIT_MET 0
METAL 99
METAL 101
METAL 119
METAL 122
METAL 238
SEQUENCE 458 AA;
                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12.
                                                                                                                                                                                   BPHA_COMTE Q46372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
SEQUENCE FROM N.A.
STRAIN-B-356;
MEDLINE-97045812; PubMed-8890734;
Sylvestre M., Sirois M., Hurtubis
                                                                               Comamonas
Bacteria;
                                                               NCBI_TaxID=285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aromatic hydrocarbons catabolism;
                                                                                                                                                                                                                                                                431
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                                                                                                                    ioxygenase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKGLLDPR-IYADQSLYELELERVFGRSWLLLGHESHVPETGDFLATYMGEDPVVMVRQK
                                                                                                                                                                                                                                                                                       AIGETSYRGFYRAYQAHVSSSNWA
                                                                                                                                                                                                                                                                                                                 HNIRNFSAGGVFEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y
                                                                                                                                                                                                                                                                                                                                        SVQRTGGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKS
                                                                                                                                                                                                                                                                                                                                                                 VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR
                                                                                                                                                                                                                                                                                                                                                                                          VRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                                                                                                                                                                                     QIPTK-GNQFRAAWGGHGSGWYVDEPGSLLAVMGPKVTQYWTEGPAAELAEQRLGHTGMP
                                                                                                                                                                                                                                                                                                                                                                                                                                              QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGMQKWVIPCNWKFAAEQFCSDMYHAGTTTHLSGILAG-----IPPEMDLSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DC-GFDKAEWGPLQARVATYKGLVFANWDVQAPDLETYLGDARPYMDVMLDRTPAGTVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKSIKVFLNQCRHRGMRICRSDAGNAKAFTCSYHGWAYDIAGKLVNVPFEKEAFCDKKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN
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                                                                            testosteroni (Pseudomonas testosteroni)
Proteobacteria; beta subdivision; Comamo
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                                                                                                                                                                                               STANDARD;
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                                                                              Comamonadaceae;
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(BY)
(BY)
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                                                                                                                              (Biphenyl
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----QERLNKEIGD
  Ahmad
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SIMILARITY).
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                                                                              Comamonas
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METAL
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shareck F., Barriault D., Guillemette I., Juteau "Sequencing of Comamonas testosteroni strain B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dioxygenase;
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00090; RNGDIOXGNASE.
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pfam; pF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U47637; AAC44526.1; -. HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- CATALTIC ACTIVITY: Biphenyl + NADH + O(2) = phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-i- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
                           357
                                                                            323
                                                                                                                                                                                                                                    248
                                                                                                                                                                                                                                                                                        218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Heterohexamer consisting of three BphA subunits BphE subunits. A ferredoxin (BphF) and a ferredoxin reduc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Biphenyl-polychlorinated biphenyl degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEV-
                     FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGETSYR 414
                                                                                                                                                                                                                                                                                        CNWKFAAEQFCSDMYHAGTMSHLSGVLAG-----LPPE---MDLTQIQLSKNG
                                                                                                                                                                                                                                                                                                                                                                                                WGPLQARVETYKGLVFANWDPEAPDLKTYLSDAMPYMDVMLDRTEAGTEAIGGIQKWVIP
                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCRHRGMRIVRSDGGNAKAFTCTYHGWAYDIAGNLVNVPFEKEAFCDKKEGDC-GFDKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYADQDLYQLELERVFGRSWLMLGHETHIPKIGDYLTTYMGEDPVIMVRQKDQSIKVFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHGDEELEQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                          --TVFPTCSFLPGINTIRTWHPRGPNEVEVWAFVLVDADAPEDIKEEFRLQNIRTFNAGG
                                                                                                                           NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAG
                                                                                                                                                                                  NQFRSAWGGHGAGWFINDSSILLSVVGPKITQYWTQGPAAEKAARRVPQLPILDMFGQHM
                                                                                                                                                                                                                                    SGMGVLWDGY-----SGVHSADLVPELMAF--GGAKQERLNKEIGDVR-ARIYRSHL
                                                                                                                                                                                                                                                                                                                                         ANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEGAGLQMT---
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IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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Pred. No. 1.5e-40;
3; Mismatches 172
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ong as its content is in no
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(BY SIMILARITY).
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STITITION REPRESENTATION OF THE PROPERTY OF TH
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15-JUL-1998 (Rel. 36, Last
15-JUN-2002 (Rel. 41, Last
Biphenyl dioxygenase alpha
                                                                                                                                                                                METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                  Dioxygenase;
                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00570: RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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Local Similarity
nes 147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Heterohexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Biphenyl-polychlorinated biphenyl degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Heterohexamer consisting of three BphA subunits and bphE subunits. A ferredoxin (BphF) and a ferredoxin reductase (BphG) must be present to obtain activity (By similarity).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
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                                                                                                                                                                                                                                                                                                                                                                       PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
S; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P23094; 1NDO.
Pro; IPR001281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001663; Ring_hydroxyl_A.
                                                                    Conservative
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102
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123
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                                                                                      25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rieske.
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IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                         Score 614;
Pred. No. 1
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                                                                    Mismatches
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01-AUG-1988
01-NOV-1988
15-JUL-1999
                                                                                                                                                                                                                                                    benzene oxidation enzymes of Pseudomonas putida.";
J. Bacteriol. 169:5174-5179(1987).
-:- CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-dihydrobenzene-1,2-diol + NAD(+).
-:- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BNZA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BNZA_PSEPU
                                                                                                                                                                                                                                                                                                                           Irie S., Doi S., Yorifuji T., Takagi M., Yano K.;
"Nucleotide sequencing and characterization of the
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88032840; PubMed=3667527;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
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                                                                                                                                                                 PATHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL. SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BNZA AND BNZB), FERREDOXIN (BNZC) AND A FERREDOXIN REDUCTASE (BNZD), SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYAEEAARGMYHHWMRMMSEPSWA
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EMBL; M17904; AAA25735 PIR; A29830; A29830.

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Best Loc
Matches
Fukuda M., Yasukouchi Y., Kikuchi Y., Nagata Y.
Horiuchi H., Takagi M., Yano K.;
"Identification of the bphA and bphB genes of P
KKS102 involved in degradation of biphenyl and
                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Biphenyl dioxygenase alpha subunit (EC 1.14
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PRINTS; PR00090; RNGDIOXYL_ALPHA; 1.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
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                                                                                SEQUENCE FROM N.A. MEDLINE=94324977; PubMed=8048958;
                                                                                                                                                             Pseudomonas sp. (strain Bacteria; Proteobacteria
                                                                                                                             NCBI_TaxID=307;
[1]
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InterPro; IPR001663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLWDGYSGVHSADLVPELMAF - - GGAKQERLNKEIGDVR - - ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
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Ring_hydroxyl_A.
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IRON-SULFUR (2FE-2S)
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Pred. No. 2.
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hes 176;
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         polychlorinated
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Biochem. Biophys. Res. Commun. 202:850-856(1994).
-!- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) -
phenylcyclohexa-3,5-dlene-1,2-diol + NAD(+).
-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
Aromatic hydrocarbons catabolism; Oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. UsentLities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-I- PATHWAY: Biphenyl-polychlorinated biphenyl degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
 412
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                                                                                                                                                                                                                                                                                                       VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEV- 138
                                                                                                                                                                                                                                                                                                                                                         SYRGFYRAYQAHVSSSNW
                                                                                                                                                                                  CNWKFAAEQFCSDMYHAGTMAHLSGVLS-----SLPPE---MDLTQVQMSKNG
                                                                                                                                                                                                                                                                                        QCRHRGMRICRSDAGNAKAFTCTYHGWAYDIAGNLVNVPYEKEAFCDKKEGDC-GFDKAD
                                                 PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGET
                                                                             --TVFPTCSFLPGINTIRSWHPRGPNEVECGPSWSSMPMR---
                                                                                                    NCTVFPNNSMLTCSGVFKVWNPIDANTTEV---WTYAIVEKDMPEDLKRRLADSVQRTGG
                                                                                                                              SQFRAAWGGHGSGWFINDAAILMAVMGPKITQYWTQGPAAEKAAKRLNQMPTQTMFGQHM
                                                                                                                                                        SGMGVLWDGYSGVHSADLVPELMAFGGAK
                                                                                                                                                                                                           ANWKAPAENFYGDAYHYG-WTHASSLRSGESIFSSLAGNAALPPEGAGLQMT----SKYG
                                                                                                                                                                                                                                       WGPLQARVETYKGLIFANWDAEAPDLKTYLSDAMPYMDVMLDRTEAGTTVVGGMQKWVIP
                                                                                                                                                                                                                                                               ----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIK 192
                                                                                                                                                                                                                                                                                                                                            IYADQDLYEIELERIFARSWLLLGHEAHIPKTGDYLTTYMGEDPVIMVRQKDGSIKVFLN
                          AGGTFEQDDGENWVEIQRGLRGHKAKSAPLCAQMGLNVPNKSNPDFP---GKTAYVYAEE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
147; Conserv
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No. 3
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les 174;
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Best Local :
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Eur. J. Biochem. 204:113-120(1992).
-1- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-1- PATHWAY: DEGRADATION OF BENZOATE AND TOLUATE TO CATECHOL.
-1- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THERE PROTEI
TWO SUBUNITS OF THE HUDROXYLASE COMPONENT (XYLX AND XYLY)
ELECTRON TRANSFER COMPONENT (XYLZ).
-1- SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neidle E.L.,
Harayama S.;
"Cis-diol deh
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01-NOV-1991
01-NOV-1991
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                           Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDTOXGNASE.
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01-NOV-1991 (Rel. 20, La
15-DEC-1998 (Rel. 37, La
Toluate 1,2-dioxygenase
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                      METAL
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                                                                                                                                                                                                                                                      PROSITE; PS00570; RING_HYDROXYL_ALPHA; Aromatic hydrocarbons catabolism; Oxid
                                                                                                                                                                                                                                                                                                                PIR; S23482; S23482.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                               or send
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the Acinetobacter calcoaceticus chromosomal
                                                                        DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR 82
                      HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKKCLG---LKEV 138
HRGATLCRFRSGNKATHTCSFHGWTFSNSGKLLKVKDPKGAGYPDSFD--CDGSHDLKKV 151
                                               DPRLFDLEMKHIFEGNWIYLAHESQIPEKNDYYTTQMGRQPIFITRNKDGELNAFVNACS 93
                                                                                                                                                                                                                                                                                                                                                       M64747; AAA26047.1;
                                                                                                               Similarity
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454 AA;
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20, Last sequence update)
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                                                                                                 Score 410.5; DE 
Pred. No. 1.2e-2 
54; Mismatches 1
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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Oxidoreductase; Iron-sulfur;
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Elby D.M., Neidle E.L.;
Submitted (DEC-2001) to the E
Submitted (DEC-2001) to the F
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P07769;
             PRINTS; PR00090; RNGDTOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
                                        Pfam; PF00355; Rieske; 1. Pfam; PF00848; Ring_hydroxyl_A;
                                                                                                  EMBL; AF009224; AAC46436.2; PIR; S23477; S23477.
                                                                                                                                                       entities requires a
                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequences of the Acinetobacter calcoaceticus for benzoate 1.2-dioxygenase reveal evolutionary relation multicomponent oxygenases.";
J. Bacteriol. 173:5385-5395(1991).
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Aromatic hydrocarbons
                                                                 InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                   PATHWAY: DEGRADATION PATHWAY LEADING FROM BENZOATE TO CATECHOL SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEINS: T TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BENA AND BENB), AND
                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                             COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM
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                                                                                                                                           s requires a license agreement (S an email to license@isb-sib.ch).
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2002 (Rel. 41, Last
2002 (Rel. 41)
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nett C., Ornston N.L.,
catabolism; Oxidoreductase;
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                                                                                             Gregor J., pu., Gregor J., shao Y.;
                                                                                                      [1]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Pernz Blattner F.R., Plunkett G. III, Bloch C.A., Pernz Riley M., Collado-Vides J., Glasner J.D., Rode C Riley M. Collado-Vides J., Glasner J.D., Goeden
                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Putative dioxygenase alpha subunit yee
YEAW OR B1802 OR Z2845 OR ECS2511.
  SEQUENCE FROM STRAIN=K12;
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15-JUL-1998
                                                                     Science
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                                                                     complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohishi M., Kurokawa K., Ishii K., Yokoy;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe 'I
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yokoy;
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000274; AAC74872.1; -
EMBL; D90823; BAA15597.1; ALT_INIT
EMBL; D90824; BAA15606.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (see or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005403; AAG56791.1; -. EMBL; AP002558; BAB35934.1; -.
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                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                          Hypothetical NAD; Complete
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00355; PROSITE; PS005
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InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- COFACTOR: PRÓBABLÝ BINDS A 2FE-2S GROUP AND AN IRON ATO
-1- SUBUNIT: PROBABLE HETERODIMER OF YEAW AND YEAX.
-1- SIMILARIY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EcoGene; EG13509; yeaW
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MEDLINE=21074935; PubMed=11206551;
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                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as los content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Choline monooxygenase, chloroplast precursor (EC 1.14.15.
                                InterPro; IPR001281; Rieske.
Pfam; PF00355; Rieske; 1.
Monooxygenase; Oxidoreductase; Chloroplast; Iron-sulfur; Iron;
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Choline + 2 reduced ferredoxin + O(2) betaine aldehyde + 2 oxidized ferredoxin + H(2)O.
-!- COFACTOR: Magnesium. Probably binds a 2Fe-25 group and an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21520075; PubMed=11642403; Meng Y.L., Wang Y.M., Zhang B., Nii N.; "Isolation of a choline monooxygenase cDNA clone from Amaranthus
                                                                                          EMBL; AF290974; AAK82768.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Leaf;
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                                                                                                                                                                                                                                                                         INDUCTION: By salt, drought and heat stress.
SIMILARITY: BELONGS TO THE CHOLINE MONOOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                    atom (By similarity).

PATHWAY: Osmoregulatory choline-glycine betaine pathway.

SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Catalyzes the first step of the osmoprotectant glycine
                                                                                                                                                                                                                                                                                                                                                                                                                       betaine synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRGKTLVSVEAGNAKGFV-CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCSGVFKVWNPIDANTTEVWTY-------AIVE--KDM--PEDLKRRLADSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGTDAAFHGFW----LWPCTM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNIVDNYL-ECYHCGPAHPGFSDSVQVDRYWHTMHGNWTLQYGFAKPSE-----QSFKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAPAENFVGDAYHVGWTHA--SSLRSGESIFSSLAGNAAL-----PPEGAGLQMTSKYG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEYAGFVFINMDPNATSVEDQLPGLGAKVLEACPEVHDLKLAARFTTRTP-----ANW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESFHGFIYGCFDQEAPPLMDYL-GDAAWYLEPM-----FKHSGGLELVGPPGKVVIKANW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRGHQLLSGE-GKAKNVITCPYHAWAFKLDGNLAHARNCENVANFDSDKAQL---VPVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334
   Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
CHLOROPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442
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                                                                                   GQGKVHAFHNVCTHRA-SILACGTGKKSCFVCPYHGWVFGLDGSLMKATKTEN---QVFD
                                                                                              NDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLN 129
                                                                                                                             AEDGFTPPSTWYTDPSLYSHELDRIFSKGWQVAGYSDQIKEPNQYFTGSLGNVEYLVCRD 153
IN-RSEFPMESNWKVFCDNYLDSAYHVPYAH
                                         PKELGLVTL-KVAIWGPFVLISLDRSGSEGTEDVGKEWIGSCA--
                                                              KKCLGLKEVARVESFHGFIYGCFDQEAPP-----LMDYLGDAAWYLEPMFKHS--GGLEL 182
                    VGPPGKVVIKANWKAPAENFVGDAYHVGWTH
                                                                                                                                                                       60;
                                                                                                                                                                                  Similarity
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167
184
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167
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187
290
295
                                                                                                                                                                                  9.9%;
                                                                                                                                                                                                                 49845 MW;
                                                                                                                                                                      39; Mismatches
                                                                                                                                                                                                                          CHOLINE MONOOXYCENASE.
IRON-SULFUR (2FE-2S) (B
IRON-SULFUR (2FE-2S) (B
IRON-SULFUR (2FE-2S) (B
IRON-SULFUR (2FE-2S) (B
IRON (POTENTIAL).
IRON (POTENTIAL).
                                                                                                                                                                                  Score 239.5;
Pred. No. 2.6
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                    213
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                                                                                                                                                                                           DB 1;
                                                                                                                                                                      96;
                                                                                                                                                                                                                                                (BY
(BY)
(BY)
                                                                                                                                                                       Indels
                                                                                                                                                                                           Length 442;
                                         - EEVKKHAFDPSLQF
                                                                                                                                                                                                                                               Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
                                                                                                                                                                       16;
                                                                                                                                                                       Gaps
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7;

Search completed: January 27, 2003, 08:59:38 Job time: 9.33333 secs

4)

Run on:	OM protein -	
January 27,	OM protein - protein search, using sw model	Copyright
2003, 08:55:37 ;	using sw model	Copyright (c) 1993 - 2003 Compugen Ltd
Search		Compuge
January 27, 2003, 08:55:37; Search time 13.1667 Seconds		en Ltd.

(without alignments)
3278.305 Million cell updates/sec

GenCore version 5.1.3

Title:
Perfect score:
Sequence:

US-09-843-250-32
2410
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28						22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	on	5	4	ω	2	_		Result
311.5	327	333.5	389.5	391	406.5	410.5	415	449	584	586.5	602	614	614	614.5	636	647.5	649.5	722.5	734	734	734	771	954	2048	2289	2343	2401	2401	90016	
	ω.	ω	6.	16.2		7		8	24.2		•	.51	.51	25.5			7.		30.5		0	2	9.	5.	<u>ب</u>	7.	9	99.6	Macci	
468	426	424	464	461	455	454	471	469	458	448	431	458	457	459	461	450	450	455	453	453	453	450	459	447	449	449	462	449	meng cu	
2	2	N	N	2	Ν	N	2	N	N	ш	ν	_	۲	44	N	ш	Н	Ν	2	N	N	2	N	N	N	N	N	N		3
G97447	T31278	E83384	G83331	S23477	E83332	A41659	T31281	T50934	JC2467	A29830	3W0098	A42409	JC4993	B41858	S51757	A36516	JN0812	T31258	G85898	D91054	A65031	T31256	T31134	JC5352	C55217	JN0644	S27632	JS0071		;
		probable ring-hydr	_	Œ	_		benzoate 1,2-dioxy	dioxygenase DitA1,	$\boldsymbol{\vdash}$		Œ			1	l dioxygen		1,2-dioxy	C				terminal oxygenase	naphthalene dioxyq	uene di	മ		naphthalene 1,2-di	ne	Description	

45	44	43	42	41	40	39	38	37	36	3 5	34	ယ	32	31	30	
186	214.5	223	224	233.5	244	244	244	248.5	260	269.5	285.5	287	291	309.5	311.5	
7.7	8.9	9.3	9.3	9.7	10.1	10.1	10.1	10.3	10.8	11.2	11.8	11.9	12.1	12.8	12.9	\
426	186	439	446	382	374	374	374	374	420	404	415	412	429	391	468	
2	N	N	2	Ŋ	N	N	2	N	2	N	Ν	N	2	N	2	
T08550	JC5354	T09214	T14542	G70946	B64941	G90942	C85791	AF0304	T31285	н87635	AG3320	H95311	F82970	T31251	AH2665	
choline monooxygen	2-nitrotoluene dio	choline monooxygen	choline monooxygen	probable dioxygena	probable choline m	probable choline m	probable choline m	probable dioxygena	biphenyl dioxygena	Rieske 2Fe-2S fami	benzoate 1,2-dioxy	probable aromatic-	probable ring hydr	aromatic oxygenase	ring hydroxylating	

ALIGNMENTS

Query Match 99.6%; Score 2401; DB 2; Length 449; Best Local Similarity 99.8%; Pred. No. 4.8e-183;
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
F;71-119/Domain: Rieske [2Fe-2S] homology <rsk></rsk>
C; Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
C:Superfamily: toluene dioxygenase terminal oxygenase component large chain: Rieske [
C;Genetics:
C; Comment: Naphthalene dioxydenase system is composed of three proteins.
A;Cross-references: GB:M23914; NID:g151392; PIDN:AAB47591.1; PID:g151394
A; Residues: 1-449 <kur></kur>
A; Molecule type: DNA
A; Accession: JS0071
A; Reference number: JS0070; MUID: 89211973; PMID: 3243438
A; Title: Cloning, nucleotide sequence and characterization of genes encoding naphthal
Gene 73, 355-362, 1988
R;Kurkela, S.; Lehvaeslaiho, H.; Palva, E.T.; Teeri, T.H.
C; Accession: JS0071
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
C; Species: Pseudomonas putida
naphthalene dioxygenase (EC 1.14.12) ndoB protein - Pseudomonas putida

Mat	Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	••
Qy	1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60	
ДЪ	1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60	
Qy	61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120	
В	61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120	
Qy	121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	
Db	121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	
Qy	181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240	
Db	181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240	
Qy	241 QMTSKYGSGMCVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300	
Db	241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300	
Qy	301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES 360	
Db	301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWES 360	
Qy	361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	

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A; Molecule type: DNA
A; Roslidues: 14-462 <DE2>
A; Reslidues: 14-462 <DE2>
A; Cross-references: GB:M60405; NID:g151195; PIDN:AAA16125.1; PID
A; Experimental source: strain C18
C; Superfamily: toluene dioxygenase terminal oxygenase component :C: Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-1; 84-132/Domain: Rieske [2Fe-2S] homology <RSK>
F; 84-132/Domain: Rieske [2Fe-2S] cluster (Cys, His, Cys, His
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Bacteriol. 175, 6890-6901, 1993
A;Title: Metabolism of dibenzothiophene and naphthalene A;Reference number: A49343; MUID:94042852; PMID:8226631
A;Accession. B49343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
$27632

s27632

naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfur oxygenase (C;Species: Pseudomonas sp.
C;Species: Pseudomonas sp.
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15
C;Accession: $27632; B49343
C;Accession: $27632; B49343
R;Denome, S.A.; Young, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-462 <DEN>
A; Cross-references: EMBL: M60405
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                   QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                               QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                               DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                              FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                                                                                        MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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Pred. No. 5e-183;
0; Mismatches
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              A;Title: Identification and characterization of genes A;Reference number: A55217; MUID:94209249; PMID:815761 A;Accession: C55217
                                                                                           polycyclic aromatic hydrocarbon dioxyge
C;Speckes: Pseudomonas putida
C;Date: 05-May-1995 #sequence_revision
C;Accession: C55217
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                                                            R;Takizawa, N.; Kaida, N.; Torigoe, J. Bacteriol. 176, 2444-2449, 1994
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A; Residues: 1-449 <SIM>
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Gene 127, 31-37,
A; Status: preliminary
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C;Superfamily: toluene dioxygenase terminal oxygenase component large chain C;Keywords: 2Fe-2S; heterotetramer; metalloprotein; oxidoreductase; Rieske F;71-119/Domain; Rieske [2Fe-2S] homology cRSK> F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pseudomonas putida
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
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                      QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                     DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                                                                                                                                                                                                                                                                        QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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                                                                                          DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                        FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWES
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QAHVSSSNWAEFEDASSTWHTELTKTTDR
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Pred. No. 2e-178;
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dioxygenase

(EC 1.14.12.-) iron-sulfur

05-May-1995 Moritani,

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A;Gene: ntdAc
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protei
F;69-117/Domain: Rieske [2Fe-2S] homology <RSK>
F;69-117/Domain: Rieske [2Fe-2S] cluster (Cys, His, Cys, His) (covalent) #
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A;Residues: 1-449 <TAK>
A;Residues: 1-449 <TAK>
A;Residues: 1-449 <TAK>
A;Residues: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
A;Cross-references: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [2Fe
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;71-119/Domain: Rieske [2Fe-2S] homology <RSK>
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status pre
                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-447 < RAR>
A; Cross-references: GB:U49504; NID:g1773273;
A; Experimental source: strain JS42
C; Comment: This enzyme catalyzes the addition
                                                                                                                                                                                                                                                                                                                                                                                    2-nitrotoluene dioxygenase (EC 1.14.12.-) iron-sulfur protein large chain N;Alternate names: 2-nitrotoluence iron-sulfur protein alpha chain C;Species: Pseudomonas sp. C;Date: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Aug-199 C;Accession: JC5352 R;Parales, J.V; Kumar, A.; Parales, R.E.; Gibson, D.T.
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83.
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94.4%; Pred. No. 3.9e-174;
tive 13; Mismatches 12;
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Score 2048; DB 2;
Pred. No. 5.7e-155;
4; Mismatches 37;
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                                                                                                                                                                                                                                                                      DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                              QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                    ELVGPPGKVVVKANWKPFAENFVGDIYHVGWTHAAALRAGQSVFSSLAGNAKLPPEGAGL
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QAHISSSNWAEFENASRNWHTELTKTTDR
                                                     DDNENMETLSQNAKKYQSSNSDQIASLGFGKDVYGDECYPGVVGKSAIGETSYRGFYRAY
                                                                                                          FPNNSFLTGSATFKVWNPIDENTTEVWTYAFVEKDMPEDLKRRLADAAQRSIGPAGFWES
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A; Description: Complete sequence of
A; Reference number: Z20992
A; Accession: T31134
A; Status: preliminary; translated f:
A; Molecule type: DNA
A; Residues: 1-459 <ROM>
A; Cross-references: EMBL: AF079317; I
C; Genetics:
                                                                                                                                                                                                                                                                              A;Gene: bphAlf
A;Genome: plasmid pNL1
A;Genome: plasmid pNL1
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;80,82,100,103/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
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                                                                          LNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK-HSGGLELVGPP
                                                                                                                         RQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGES
                                             LDKSKLGLAPI-RVETYKGFIFGCHDPEAPSLEDYLGDFCWYLDTIWDGPDGGLELLGPP
                                                                                                        RQPDGSLKAFINSCTHRGNQICHADSGSAKAFVCNYHGWVFGQDGSLVDVPMEERCYHSD
                                                                                                                                                                                                                                                                                                                                                                                EMBL:AF079317; NID:g3378261; PID:g3378275; PIDN:AAD03858
                                                                                                                                                                                                                                           39.68;
                                                                                                                                                                                                                                          Score 954; DB 2
Pred. No. 6e-68;
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                                                                                                                                                                                                                                                           DB 2;
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PID:g17888

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terminal oxygenase component large chain homolog - Sphingon C: Species: Sphingomonas aromaticivorans C: Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_cl C: Accession: T31256
R: Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J submitted to the EMBL Data Library, July 1998
A: Description: Complete sequence of a 184 kb catabolic plase A: Reference number: Z20992
A: Accession: T31256
A: Reference number: translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-450 < ROM>A: Residues: 1-450 < ROM>A: Residues: 1-450 < ROM>A: Cross-references: EMBL: AF079317; NID:g3378261; PID:g3378: C: Genetics:
A: Genome: plasmid pNL1
A: Mole: bphAla
C: Superfamily: toluene dioxygenase terminal oxygenase compo C: Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur prof F:81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys)
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                         LFDNDDGDNLTACTEQSRGWRTAQMDVYTNMALGRSGKREG-FPGDIAAGLVSEHNQRYF
                                                                 FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGF
                                                                                                              NITIFPNLQLLPGLNWFRVYHPKGPGQIEQWTWAMAENDMPEAVKAQILENQCLTFGLAG
                                                                                                                                                      NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAG
                                                                                                                                                                                                       -GLSVAGMNGHMVLSALDGVSGYAFYPDPKPILEYLEANRQTVIDRLGEVRGRQVWGAQV
                                                                                                                                                                                                                                               AGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHL
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36.1%;
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65031
A;Status: preliminary; nucleic acid sequence not shown; tr
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A;Molecule type: DNA
A;Residues: 1-19,'A',21-383,'ATAPATANCYWKW',397-398,451,'R',453,'SAATTAFLALLTISFOKLPL
A;Cross-references: EMBL:237966; NID:g550595; PIDN:CAA86018.1; PID:g550596
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;75-123/Domain: Rieske [2Fe-2S] homology CRSK>
F;85,87,105,108/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
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A;Description: Cloning and sequencing of an E. coli gene homologous
A;Reference number: S49292
A;Accession: S49292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain K-12, s R; Turlin, E.; Gasser, F.; Biville, F.
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
C;Accession: A65031; S49292
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A; Residues: 1-453 <BLAT>
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                                                                                                           YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                                                  GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
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                                                                 ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK 453
                                                                                                                                                          GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA
                                                                                                                                                                                                                                                                                             RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTG
                                                                                                                                                                                                                                                                                                                                          QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----AEQRLGEVRALRL
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64; Mismatches
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RESULT 10

G85898

G85898

biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain - Es. C; Species: Escherichia coli
C; Species: 16.Feb-2001 #sequence_revision 16.Feb-2001 #text_change 31.Dec-2001
C; Accession: G85998
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-453 <STO>
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A;Gene: ECs3404
C;Superfamily: toluene dioxygenase terminal oxygenase component 1 C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D91054 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-453 <HAY>
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 *sequence_revision
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N.; Yasunaga, T.; Kuhara, S.;
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Pred. No. 1.8e-50;
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Shiba, T.; Hat
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Shinagawa,
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83 61

N

Matches

Similarity

Conservative

83;

169;

19;

Gaps

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A; Note: bphAlb
C; Superfamily: 1
C; Keywords: 2Fe
F; 88, 90, 108, 111,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: hcaA1
C;Superfamily: toluene dioxygenase terminal
C;Keywords: oxidoreductase
                                                                                                                                                 A; Genome:
                                                                                                                                                              C; Genetics:
                                                                                                                                                                               A; Cross-references: EMBL: AF079317; NID: g3378261; PID: g3378399; PIDN: AAD03982.1
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-455 < ROM>
                                                                                                                                                                                                                                    A; Status: preliminary; translated
                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T31258
                                                                                                                                                                                                                                                                          R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, submitted to the EMBL Data Library, July 1998 A;Description: Complete sequence of a 184 kb catabolic A;Reference number: Z20992
                                                                                                                                                                                                                                                                                                                                                  C; Accession: T31258
                                                                                                                                                                                                                                                                                                                                                                 C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000
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Best Local S
Matches 165
                                                                  Superfamily: toluene dioxygenase terminal oxygenase component large chain; Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein; Reywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein; 88,90,108,111/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                    Query Match
Best Local
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Pred. No. 1.8e
64; Mismatches
Score 722.5; DB 2
Pred. No. 1.5e-49;
3; Mismatches 169
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RESULT 12

Denzene 1,2-dioxygenase (EC 1.14.12.3) terminal oxygenase component large chain - Pseudo
C:Species: Pseudomonas putida
C:Species: Pseudomonas putida
C:Accession: JN0812
R:Tan, H.M.; Tang, H.Y.; Joannou, C.L.; Abdel-Wahab, N.H.; Mason, J.R.
Gene 130, 33-39, 1993
A:Title: The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenase are un
A:Reference number: JN0810; MUID:93345820; PMID:8344526
A:Molecule type: DNA
A:Accession: JN0812
A:Cross-references: GB:L04642; GB:L04643; NID:g6552505; PIDN:AAA17758.1; PID:g309855
A:Experimental source: Strain ML2
C:Comment: This enzyme is involved in catalyzing the oxidation of benzene to cis-1,2-dif
C:Genetics:
A:Gene bedC1
A:Genemetics: Zee-zs; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; Rie
C:Keywords: Zee-zs; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; Rie
F:96,98,116,119/Binding site: ZFe-2S cluster (Cys, His, Cys, His) (covalent) #status pre
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WKAPAENEVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
                                                   PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
                                                                                    --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                         QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA----
                                                                                                                                                        VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                             IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
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                                    TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS
                                                                                                                                                                                                                                                                                                   --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                                                                                                                                                                                                                                                                               VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IHGDEELFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLN
                  EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP
                                                                                                          TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWESDDNDNME
                                                                                                                                                          GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
                                                                                                                                                                                            VLWDGYSGVHSADLVPELMAF -- GGAKQERLNKEIGDVR -- ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                               WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                                                                                                                                                                                                                                              WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                                                                                                                         QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
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                                                                                    PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
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94 79

441

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A:Gene: todCI
c;Superfamily: toluenc dioxygenase terminal oxygenase component large chain; Rieske C;Superfamils: Tele-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; C;Keywords: 2Fe-2S; homology <RSK>
F;86-134/Domain: Rieske [2Fe-2S] homology <RSK>
F;96,98,116,119/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
                                                                                                                                                                                                                          A;Cross-references: GB:J04996; NID:g151600; PIDN:AAA26005.1; A;Experimental source: strain F1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                  R;Zylstra, G.J.; Gibson, D.T.
J. Biol. Chem. 264, 14940-14946,
A;Title: Toluene degradation by F
A;Reference number: A36516; MUID:
A;Accession: A36516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pseudomonas putida C;Species: Pseudomonas putida C;Date: 15-Feb-1991 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999 C;Accession: A36516
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                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGENWYEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
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     Conservative
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                            26.9%;
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MUID:89359301; F
     71;
Score 647.5; DB 1;
Pred. No. 1.4e-43;
71; Mismatches 181;
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РМІD:2670929
     Indels
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RESULT 15
B41858
biphenyl dioxygenase (EC 1.14.12.-) te
C;Species: Pseudomonas sp.
C;Date: 04-Mar-1993 #sequence_revision
C;Accession: B41858
R;Erickson, B.D; Mondello, F.J.
J. Bacteriol. 174, 2903-2912, 1992
A;Title: Nucleotide sequencing and tra
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S51757
Siphenyl dioxygenase (EC 1.14...) large chain - Rhodococcus globerulus C;Species: Rhodococcus globerulus C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999 C;Accession: S51757
R;Asturias, J.A.; Diaz, E.; Timmis, K.N. submitted to the EMBL Data Library, July 1994
A;Description: Evolutionary relationship of the biphenyl dioxygenase of the A:Reference number: S51757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: bphAl
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;89-137/Domain: Rieske [2Fe-2S] homology <RSK>
F;99,101,119,122/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #statu
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A; Residues: 1-461 <AST>
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                                                         Date: 04-Mar-1993 #sequence_revision
Accession: B41858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMGIDEVIVSRQNDGSIRAFLN
                                                                                                                                                                                                                                            SSNWAEFEHASSTWHTELT
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                                                                                                                                                                                                                                                                                                      METASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVS
                                                                                                                                                                                                                                                                                                                                                      FLPGINTIRTWHPRGPHEIEVWSFTVVDADAPAEIKEEYRRQTIRTFSAGGVFDQDDGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                             GHGSGFYIGEMGTLAAVMGMKILEYYTSGPAAEKAAKRLGSAVRGSQATGQHMTVFPTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGMGVLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVRARIYRSHLNCTVFPNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAEQFCSDMYHVGTTSHLSGLLAG - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCRHRGMRICRADGGNAKSFTCSYHGWAYDSAGNLVSVPFQQEAFPD-LKKEDWGPLK--
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Pred. No. 1
                                                                                                             terminal
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                                                                       06-Jan-1995 #text_change
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1.2e-42;
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Search completed: January 27, Job time : 14.1667 secs

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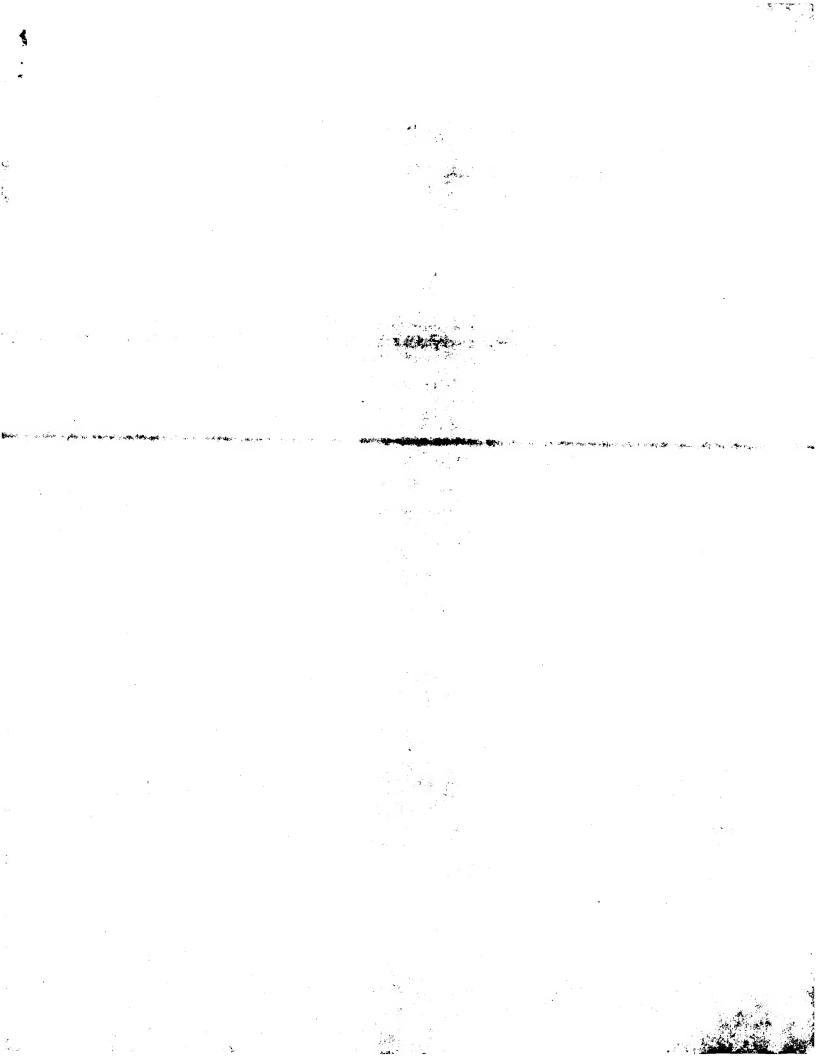
09:03:45

transcriptional mapping of the

genes encoding

bipheny

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A;Gene: bphA1; bphA
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase;
F;90-138/Domain: Rieske [2Fe-2S] homology <RSK>
F;90-138/Domain: Rieske [2Fe-2S] homology <RSK>
F;100,102,120,123/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #stat
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A;Accession: B41858
A;Accession: B41858
A;Accession: B41858
A;Residues: 1-459 <ERI>
A;Cross-references: GB:M86348; NID:9349602; PIDN:AAB63425.1; PID:g151084
A;Experimental source: Strain LB400
A;Note: Sequence extracted from NCBI backbone (NCBIN:97256, NCBIP:97259)
C;Genetics:
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  432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
VYAEEAARGMYHHWMRMMSEPSWA
                                          AIGETSYRGFYRAYQAHVSSSNWA
                                                                                                                                                                       VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR
                                                                                                                                                                                                               VRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                         QIPTK-GNQFRAAWGGHGSGWYVDEPGSLLAVMGPKVTQYWTEGPAAELAEQRLGHTGMP
                                                                                                                                                                                                                                                                                                                                                                                    GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                              DC-GFDKAEWGPLQARVATYKGLVFANWDVQAPDLETYLGDARPYMDVMLDRTPAGTVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKSIKVFLNQCRHRGMRICRSDAGNAKAFTCSYHGWAYDIAGKLVNVPFEKEAFCDKKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKGLLDPR-IYADQSLYELELERVFGRSWLLLGHESHVPETGDFLATYMGEDPVVMVRQK 89
                                                                                    HNIRNFSAGGVFEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y
                                                                                                                               SVQRTGGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKS
                                                                                                                                                                                                                                                                                                   QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAK------QERLNKEIGD
                                                                                                                                                                                                                                                                                                                                              GGMQKWVIPCNWKFAAEQFCSDMYHAGTTTHLSGILAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 614.5; DB Pred. No. 6e-41;
  455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                      431
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                                                                                                                                                                                                                                                                                                                                                                                                                              208
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on:

January 27, 2003, 08:46:47; Search time 29.1667 Seconds (without alignments)

2051.298 Million cell updates/sec
```

Scoring table: BLOSUM62 Gapop 10.0	Title: US-09 Perfect score: 2410 Sequence: 1 MNY
BLOSUM62 Gapop 10.0 , Gapext 0.5	US-09-843-250-32 2410 1 MNYNNKILVSESGLSQKHLIAEFEHASSTWHTELTKTTDR

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

908470 seqs, 133250620 residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_101002:*

1: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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6: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
7: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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23: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
23: \SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	9	8	7	6	51	4	ω	2	1	Result No.
2400	2400	2401	2401	2401	2401	2402	2402	2404	2410	Score
99.6	99.6	99.6	99.6	99.6	99.6	99.7	99.7	99.8	100.0	Query Match 1
449	449	449	449	449	449	449	449	449	449	Length DB
21	21	21	21	21	21	21	21	21	21	BOB
AAB12582	AAB12581	AAB12577	AAB12567	AAB12566	AAB12565	AAB12583	AAB12580	AAB12579	AAB12578	ID
Naphthalene dioxyg	Naphthalene dioxyq	Naphthalene dioxyq	NDO related comple	NDO related comple	Naphthalene dioxyg	Naphthalene dioxyq	Naphthalene dioxyq	10	Naphthalene dioxyq	Description

PT

Novel naphthalene dioxygenase mutant having a specific amino acid

45	44		42	41	40	39	38	37	36	35	34	ဒ္	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
126	164	173	181	181	186	196	223	224	233	235	235	239	333.5	357	376	377.5	551.5	612	615		658.5	\sim	734	1092	1965.5	2049	2186	2216	2289	2315	2343	2391	2396	2396
5.2	6.8	7.2	7.5	7.5					٠	9.8	9.8	9.9	13.8	14.8	15.6	15.7	•	25.4	25.5	•	•	•		•	81.6	•	90.7	•	95.0		87.2	. `	99/4	
405	35	35	1193	35	426	99	439	446	438	433	433	435	424	497	490	385	427	458	458	459	898	443	453	452	451	447	447	449	449	4	4		449	448
19	19	19	22	19	23	23	19	19	23	22	22	22	22	22	22	22	14	21	21	16	21	23	22	21	21	21	21	21	21	21	21	21	21	21
AAW80332	AAW79020	01	ABG18089	AAW79018	ABB93163	w	56	AAW69563	ABB06798	AAG62635	AAG62633	AAG62634	AAU33601	AAB79227	AAG92386	AAU36099	AAR32085	AAY81989	AAY81990	AAR66729	AAY83939	AA017350	AAU34660	AAB29474	AAB12576	57	AAB12574	ū	57	25	57	256	ū	AAB12584
Oxidase amino acid	Rieske motif in DN	moti	Novel human diagno	Rieske motif in 98	Herbicidally activ	Human oxygenase-li	Spinach choline mo	Sugarbeet choline	Atriplex hortensis	C album choline mo	C album choline mo	C album choline mo	Pseudomonas aerugi	Corynebacterium gl	C glutamicum prote	-	Benzene dioxygenas		Chimeric PCB decom		Benzene ring hydro	~	E. coli cellular p	kholderia		comp		_	NDO related comple	related	related	related	compl	Naphthalene dioxyg

ALIGNMENTS

DR DR	XX	ΡI	X	PA	XX	PR	XX	ΡF	XX	PD	XX	ΡN	XX	SO	SO	XX	KW	KW	ΚW	XX	DE	XX	DT	XX	AC	XX	ID	AAB125	1
WPI; 2000-452174/39. N-PSDB; AAA65352.		Parales R, Gibson D, Resnick S, Lee K;		(IOWA) UNIV IOWA RES FOUND.		26-OCT-1998; 98US-0105575.		26-OCT-1999; 99WO-US25079.		29-JUN-2000.		WO200037480-A1.		Synthetic.	Pseudomonas sp.		polymer; resin; pharmaceutical; rubber industry; bioremediation.	inducible multi-component enzyme; alpha subunit; mutant; chiral diol;	Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO;		Naphthalene dioxygenase mutant F352G protein sequence SEQ ID NO:32.		09-NOV-2000 (first entry)		AAB12578;		AAB12578 standard; Protein; 449 AA.	RESULT 1	

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RESULT 2
AAB12579
ID AAB1
XX
AC AAB1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,
                                                         AAB12579 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                             421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG 60
                                                                                                                                                                                                          QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                             DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                              DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity 449; Conserv
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                                                         Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No. 1.4e-224;
; Mismatches 0;
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                                                                                                                                                                                                                                                   CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydroxaphthalene, which cc involves contacting them with naphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydroxphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-c dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-c dihydroxy-1,2-dihydroxy-1,2-c dihydrophenanthrene which converted the most cells are also used in bioremediation in which they oxidise an example compound such as indene, 1,2-dihydronaphthalene, oxidise an cc aromatic compound such as indene, 1,2-dihydronaphthalene, c benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, cc dibenzothiophene, 9,10-dihydroxy transphthalene, biphenyl, fluorene, dibenzofuran, cc dibenzothiophene, 9,10-dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cc resin, pharmaceutical or rubber industry. The present sequence represents anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the cx exemplification of the present invention.
                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1S,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol,
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                                                                                                     KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                     IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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448; Conserv
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                                                                                                      The present invention describes a naphthalene dioxygenase (NDO) or N related complex (I) comprising several polypeptides which contain an related complex (I) comprising several polypeptides which contain an related amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(IS,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
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involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxphenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which
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                                                                                                                                                                                                 dioxygenase mutant F352W
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99WO-US25079
                                                                                                                                                      .-component
                                                                                                                                                    strain NCIB 9816-4; naphthalene dioxygenase; component enzyme; alpha subunit; mutant; chi
                                                                                                                                    pharmaceutical; rubber industry;
                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                               protein sequence
                                                                                                                                    mutant; chiral bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                        QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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Pred. No. 8.2e-224;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 449;
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                                   CC dilydroxy1nda, 1,2-dilydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dilydronaphthalene respectively. The polypeptides and CC the host cells are also useful for preparing 1,2-dilydroxy-1,2-CC dilydroxy-1 contacting them with phenanthrene. The polypeptides and the lost cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dilydronaphthalene, CC benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, CC acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, CC dibenzothiophene, 9,10-dilydroanthracene, or 9,10-dilydrophenanthrene a corresponding dilydro dilydroxy compound. The polypeptides and the host C cells are useful for preparing chiral diols for use in the polymer, CC resin, pharmaceutical or rubber industry. The present sequence represents anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mutant alpha subunit, given in the corresponding dilydropenase (NDO) mu
                                                                                                                                                                                                                                                                                                                                                                                                                               alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 58-60; 151pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes a naphthalene dioxygenase (NDO) or NDO ated complex (I) comprising several polypeptides which contain an
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                          Claim 13;
                                                                                           Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
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                                                                                                                                                                                                                                                                                                                                            cc related complex (I) comprising several polypeptides which contain an C alpha subunit that contains substituted amino acids at specific C positions. The polypeptides and host cells are useful for preparing C (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-C dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cinvolves contacting them with naphthalene, biphenyl, phenanthrene, C indene, and 1,2-dihydronaphthalene respectively. The polypeptides and C the host cells are also useful for preparing 1,2-dihydroxy-1,2-C dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which convolves contacting them with phenanthrene. The polypeptides and the convolves contacting them with phenanthrene. The polypeptides and the convolves contacting them with phenanthrene, which they oxidise an cc aromatic compound such as indene, 1,2-dihydrophenanthrene which convolves contacting them with phenanthrene, dibenzo(1,4)dioxan, C decaphthylene, naphthalene, phenanthrene, dibenzo(1,4)dioxan, C dibenzothyophene, 9,10-dihydropanthracene, dibenzo(1,4)dioxan, C dibenzothophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host C cells are useful for preparing chiral diols for use in the polymer, C anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the c exemplification of the present invention.
                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 100-102; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-452174/39.
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polymer; resin; pharmaceutical; rubber industry; bioremediation.
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                                                                                                                                  ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                               KDLYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
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Pred. No. 16
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RESULT 8
AAB12577
The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (I) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)-(15,2R)-cis-naphthalene dihydrodiol, (-or+)-cis-biphenyl-3,4-CC dihydroxyindan, 1,2-dihydroxyindan, 1,2-dihydroxyindan, 1,2-dihydroxyl-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydronaphthalene respectively. The polypeptides and CC dihydrophenanthrene or 3,4-dihydroxy-1,2-1,2-dihydroxy-1,2-CC dihydroxy-1,2-dihydroxy-1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which convolves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an CC involves contacting them with phenanthrene. The polypeptides and the CC host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, CC benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, CC acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, CC dibenzothiophene, 9,10-dihydroxy compound. The polypeptides and the host CC corresponding dihydro dihydroxy compound. The polypeptides and the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel naphthalene dioxygenase mutant having a specific amino substitution for preparing chiral diols for use in the polyme pharmaceutical or rubber industry and for carrying out bioren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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Best Local
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                                                                                                                                                                                                                                    09-NOV-2000
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                                                  26-OCT-1998;
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                                                                                                                WO200037480-A1
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The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (1) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (1)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cis-1,2-CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which clindene, and 1,2-dihydronaphthalene, perpendictly. The polypeptides and CC involves contacting them with naphthalene, biphenyl, phenanthrene which they dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-CC dihydroxy-1s are also used in bioremediation in which they oxidise and the const cells are also used in bioremediation in which they oxidise and CC involves contacting them with phenanthrene. The polypeptides and the const cells are also used in bioremediation in which they oxidise an caromatic compound such as indene, 1,2-dihydronaphthalene, compound such as indene, 1,2-dihydronaphthalene, compound such as indene, phenanthrene, dibenzo(1,4)dioxan, compound such as indene, phenanthrene, dibenzo(1,4)dioxan
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449 AA;
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                                                                DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                                                                                 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
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                                                                                                                                                                                                                   exemplification
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                                                                                                                         alene dioxygenase mutant having a specific for preparing chiral diols for use in the all or rubber industry and for carrying out
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The present invention describes a naphthalene dioxygenase (NDO) or N related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1s,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1s,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodyl, 1,2-dihydrodyl, 1,2-dihydroxylndan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which

Example

7; Page 144-145; 151pp; English.

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ID ARBI2
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Best Local
                                                                                                                                                                       Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d
                                                                                                                                                                                                                                                                                                                         09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB12568 standard; Protein;
                                                                                                                                              polymer;
                                                                                                                                                                                                                                                                  NDO related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAHVSSSNWAEFEHASSTWHTELTKTTD 448
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                                                                                                                                                 resin;
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                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                              pharmaceutical;
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Pred. No. 3.1e-223;
                                                                                                                                                 rubber industry;
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                                                                                                                                              mutant; chiral bioremediation
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dihydroxyindan, 1,2 dihydroxy-1,2,3,4-tetrahydronaphthalene, which convolves contacting them with naphthalene, biphenyl, phenanthrene, contacting them with naphthalene, biphenyl, phenanthrene, contacting them with naphthalene, long them yellowed the host cells are also useful for preparing 1,2-dihydroxy-1,2-convolves contacting them with phenanthrene. The polypeptides and the linvolves contacting them with phenanthrene. The polypeptides and the constructing them with phenanthrene. The polypeptides and the lost cells are also used in bioremediation in which they oxidise an constitution of the properties and the linvolves compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, consequence, naphthalene, biphenyl, fluorene, dibenzofuran, consequence, phenanthrene, dibenzofuran, conversional dihydro dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host corresponding dihydro dihydroxy compound. The polypeptides and the host corresponding dihydro dihydroxy compound. The polypeptides and the host corresponding dihydro dihydroxy compound. The polypeptides and the host corresponding dihydro dihydroxy compound. The polypeptides and the host corresponding dihydro dihydroxy compound alois for use in the polymer, cresin, pharmaceutical or rubber industry. The presents sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the corresponding dihydroxy compound in the polymer.
    Query Match
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                                                                                                Sequence
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Length 449;
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                                                     QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
FPNNSMLTCSGVEKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                               QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                            ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFCSLAGNAALPPEGAGL
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Pred. No. 3.1e-223;
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                                                  aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, dibenzothophene, 9,10-dihydronathracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15.2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 104-105; 151pp; English
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Sequence

Novel naphthalene dioxygenase mutant having a specific amino substitution for preparing chiral diols for use in the polyme pharmaceutical or rubber industry and for carrying out biorem

polymer, resin bioremediation

acid

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RESULT 14
AAB12570
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Best Local Similarity
Matches 446; Conserv
                                 N-PSDB;
                                                           Parales
                                                                                              26-OCT-1998;
                                                                                                                                                  WO200037480-A1
                                                                                                                                                                   Synthetic
                                                                                                                                                                           Pseudomonas sp
                                                                                                                                                                                           Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                   AAB12570 standard; Protein;
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                                                                                                               26-OCT-1999;
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                                                                                                                                                                                                                                 NDO related
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DB; AAA65344.
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                                                                                                                                                                                                                                                                                                                                                                           DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                          Gibson D,
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                                                                                                                                                                                                                               alpha
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Pred. No. 9.
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Best Local Sim
Matches 434;
09-NOV-2000
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                                       AAB12571 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                    QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                               QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                         QAHVSSSNWAEFEDASSTWHTELTKTTDR 449
                                                                                                                                                     DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                  QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGSKQERLNKEIGDVRARIYRSHLNCTV
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                                        Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                    97.28;
96.78;
                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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Pred. No. 4.3e-218;
"" wismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
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cc related complex (I) comprising several polypeptides which contain an C alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydroxphthalene respectively. The polypeptides and CC the host cells are also useful for preparing 1,2-dihydroxy-1,2-CC dihydroxphenanthrene or 3,4-dihydroxy-3,4-dihydroxphenanthrene which CC host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, CC benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, CC dibenzothiophene, 9,10-dihydroxanthracene, dibenzo(1,4)dioxan, CC dibenzothiophene, 9,10-dihydroxanthracene, dibenzofuran, CC dibenzothiophene, 9,10-dihydroxanthracene, dibenzofuran, CC corresponding dihydro dihydroxy compound. The polypeptides and the host CC cells are useful for preparing chiral diols for use in the polymer, CC anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC a maphthalene dioxygenase (NDO) mutant alpha subunit, given in the
                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 107-109; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-452174/39.
N-PSDB; AAA65345.
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                             61
                                                                                        <u>_</u>
                                                                                    MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
IDEVIYSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHCWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                 al Similarity
429; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e multi-component enzyme; alpha subunit; mutant; chiral
resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                          449 AA;
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                                                                                                                                                                                                                                              96.1%;
95.5%;
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                                                                                                                                                                                                                                        Score 2315; DB 21; Pred. No. 2.2e-215;
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                                                                                                                                                                                                                                                                        Length 449;
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Search completed: January 27, 2003, 08:58:47 Job time: 31.1667 secs

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Database :
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                    Published_Applications_AA: *

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *

12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep: *

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep: *

14: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep: *
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Gapop 10.0 , Gapext 0.5
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2408
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	0	G	4	ω	2	ب	Result No.
108	108	108	108	109	109	110	110	118.5	168	168	174	174	185	185	336.5	375	375.5	735	Score
4.5	4.5	4.5	4.5	4.5	4.5	4.6	4.6	4.9	7.0	7.0	7.2	7.2	7.7	7.7	14.0	15.6	15.6	30.5	Query Match Length DB
35	35	35	35	35	35	35	35	354	ၾ	35	35	35	35	35	424	490	385	453	ength I
10	10	10	10	10	10	10	10		10	10	10	10	10	10	10	9	10	10	BC BC
US-09-776-491-15	US-09-776-491-13	US-09-776-490-15	US-09-776-490-13	US-09-776-491-14	US-09-776-490-14	US-09-776-491-12	US-09-776-490-12	US-08-976-063C-4	US-09-776-491-21	US-09-776-490-21	US-09-776-491-20	US-09-776-490-20	US-09-776-491-19	US-09-776-490-19	US-09-815-242-5097	US-09-738-626-6140	US-09-815-242-11692	US-09-815-242-10253	ID
15,	13,	Sequence 15, Appl	Sequence 13, Appl	Sequence 14, Appl	Sequence 14, Appl	`	Sequence 12, Appl	Sequence 4, Appli	Sequence 21, Appl	`	Sequence 20, Appl	20,	•	Sequence 19, Appl	Sequence 5097, Ap	Sequence 6140, Ap	Sequence 11692, A	Sequence 10253, A	Description

Query Match Best Local Similarity

30.5%;

Score 735; DB 10; Pred. No. 1.4e-57;

Length 453;

ALIGNMENTS

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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILLNG DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/235,625 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR APPLICATION PRIOR APPLICATION NUMBER: 60/253,625 PRIOR APPLICATION PRIOR PRIOR APPLICATION PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR
; ORGANISM: Escherichia coli
US-09-815-242-10253
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US-09-815-242-10253
                                                                                                                                                                                                    PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10253
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APPLICANT:
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                                                                                               LENGTH: 45
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Yamamoto, Robert T.
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Matches

165;

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US-09-815-242-11692

; Sequence 11692, Application US/09815242

; Patent No. US20020061569A1
                                         NUMBER OF SEO ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11692
LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                         PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----AEQRLGEVRALRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
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Yamamoto, Robert T.
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pneumoniae
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                                                                                                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6140
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US-09-738-626-6140
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                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                          SEQ ID NO 6140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6140, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                         Query Match
                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 ---WTHASSL--RSGESIFSSLAGNAALPPEGAGLQMTSKYG--SGMGVLWDGYSGVHSA
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                                                                                  20 IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKD-LYGESLNKK-CLGLKE 137
                                         IFTDPEIFELEMRHIFEGNWIYLAHESQIPNAGDYFTTYIGRQPIMITRSKDGTLNCLIN 86
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                                                                                                                                Conservative
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                                                                                                                            15.6%; Score 375; DB 9; I
26.3%; Pred. No. 1.6e-25;
46: Mismatches 215;
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APPLICANT:

Wall, Daniel

APPLICANT: APPLICANT: APPLICANT:

H. Howard

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                                 Query Match
Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5097
LENGTH: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5097, Application Patent No. US20020061569A1
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                   PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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  25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-10-23
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Zyskind, Judith W.
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                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert T.
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27.3%;
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                                       Score 336.5; DB 10;
Pred. No. 3.5e-22;
0; Mismatches 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application Uppatent No. US20010012886A1 GENERAL INFORMATION:
                                                                                                 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 EILESCQ---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREW 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 DNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLAI
MOLECULE TYPE: protein
                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SPILLII, W. MURTAY
REGISTRATION NUMBER: 32, 9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 28234
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Briggs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS-----ADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPN--- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAKVCAERQGNSQRFTCPYHGWTYDSHGSLIGLP-DKAAYQHA--GQCHPELSLTQVKHA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGV-DAYHLPFAHKRYLEYLNTL------GTDPESHKRHGRG-EALGNGHALI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VYRNFLFIHYGARQASLETYLGQAKDYIDLICDQSEAELEIIPGGFEHSIKANWKLLAE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKC---LGLKEVARV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                  STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                          TYPE: amino acid
                                                                                                                                       TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Charlotte STATE: No. US20010012886Alth Carolina
                                                                          LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. Drawer 34009
                                                                                                                                                          ELEFAX:
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                                                                                                                                                          919-881-3175
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Gurmukh S.
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RESULT 7
US-09-776-490-20
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US-09-776-491-19
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Patent No. US20010013135A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
Gray, John
      Sequence 20, Application U Patent No. US20010012886A1
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Best Local Similarity
Matches 33; Conserv
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Best Local 9
                                                                                                                                                                                                         Matches
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECHMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPHONE: 919-881-3175
                                                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                          Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: 
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    CURSOFTIANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                           NVCRHRGKTLVSVEAGNAKGPVCSYHGWGFGSNGK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                         Conservative
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                        US/09776490
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Pred. No. 2.9e-10;
1; Mismatches 1;
                                                                                                                                                                                                                        Score 185; DB 10;
Pred. No. 2.9e-10;
                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                          Length 35;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-09-776-490-20
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
Gray, John
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INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORRESY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                             COUNTRY: USA
                                                                                                                       ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009 CITY: Charlotte STATE: No. US20010012886A1
                                                                                  STATE: No.
                                                                                                    CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 35 amino acids
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Gray, John
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                                                                                  US20010013135Alth Carolina
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                                                                                                                                                                                  CELL DEATH AND DISEASE RESISTANCE IN PLANTS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 174; DB 10;
Pred. No. 2.7e-09;
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US-09-776-490-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenttn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/776,490
FILING DATE: 02-Feb-2001
FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                   APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                           NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                            US20010012886Alth Carolina
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85.7%;
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Pred. No. 2.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
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; STRANDEDINES: CURKNOWN>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-776-491-21
Query Match
Best Local Similarity
"~+~hes 28; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-776-490-21
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US-09-776-491-21
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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|||||||||:||:
1 NVCRHRGKTIVDAEAGNAKGPVCGYHGWGYGSNGK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 65
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                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Drawer 34009
CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                              LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 35 amino acids
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                Conservative
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80.0%;
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                                 Score 168; DB 10;
Pred. No. 9.4e-09;
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Pred. No. 9.4e-09;
                  Mismatches
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                                                  DB 10; Length 35;
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                Indels
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Best Local S
Matches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexander Steinbuchel; Horst Priefert; Jurgen TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF INVENTION: CONIFERYL ALCOHOL, CONIFERYLALDEHYDE, TITLE OF INVENTION: ACID AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bay
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 196
FILING DATE: 29-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,063C
FILING DATE: 21-NOV-1997
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PRIOR APPLICATION DATA:
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208 L 208
                                      240 L 240
                                                                          149 DNLM-DLTHETYVHASSIGQKEIDEAPVSTRVEGDTVITSRYMDNVMAPPFWRAALRGNG 207
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OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                     / Match 4.9%; Score 118.5; DB 1; Local Similarity 23.2%; Pred. No. 0.0065; nes 56; Conservative 40; Mismatches 78;
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                                                                                                                                                                                                                                                                          92
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CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                 34 IFARN--WLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (914) 332-1844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                        MFPKNAWYVACTPDEIADKP---LGRQICNEKIVFYRGPEGRVAAVEDFCPHRGAPL--- 54
                                                                                                                   ENFVGDAYHVGWTHASSLR----
                                                                                                                                                       ERYGFIWVWPGDRELADPALIHHL---EWADNPEWAYGGGL-----YHIACDYRLMI 148
                                                                                                                                                                                                                                  ----SLGFVRDGKLICGYHGLEMGCEGKTLAMP------GQRVQGFPCIKSYA-VE 99
                                                                                                                                                                                         SFHGFIY---GCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPA 199
                                                                                                                                                                                                                                                                    EAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLG---LKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVCRHRGKTIVDAEAGNAKGPVCGYHGWGYGSNGK 35
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10591-5144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H: 354 amino acids
amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Diskette,
HP VECTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPRUNG KRAMER SCHAEFER & BRISCOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 49 655.1 (Germany)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.50 inch, 2.0 MB storage
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                                                                                                                 -SGESIFSS-LAGNAALPP-----EGAG
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 354;
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OF
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                         14;
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US-09-776-491-12
; Sequence 12, Ap
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US-09-776-490-12
                                                                                                                                                                   Sequence 12, Application US/09776491
Patent No. US20010013135A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                            1 NQCRHRGMRICRADAGNAKAPTCSYHGWAYDTAG
            NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                           APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35 amino acids
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                                                                        CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 08/810,009
FILING DATE: 04 -MAR-1997
ATTORNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELEPRENCE/DOCKET NUMBER: 5718-4
TELEPRENCE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                             Gray, John TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US20010012886Alth Carolina
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                       PARK & GIBSON
                                                                                          AND DISEASE RESISTANCE IN PLANTS
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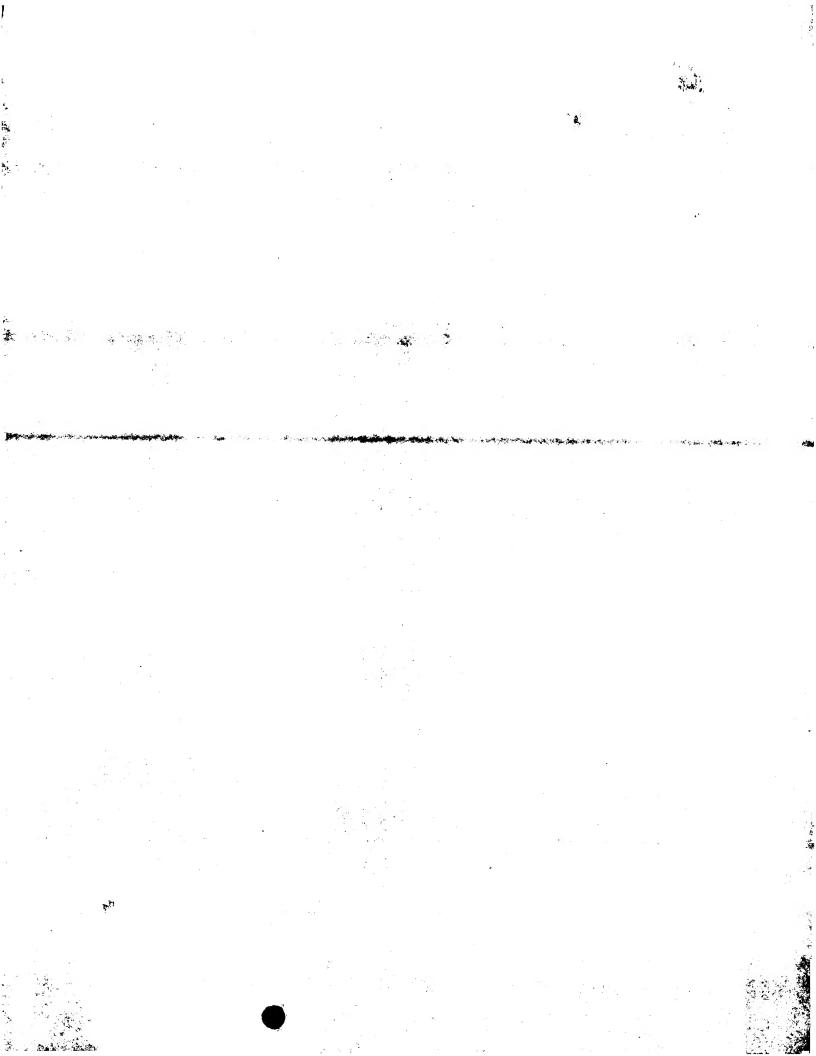
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RESULT 14
US-09-776-490-14
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Matches 18; Conservative
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NOCKHRÖMRICRADAGNAKAPTCSYHGWAYDTAG 34
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/776,491
ETILING DATE: 02-Feb-2001
CLASSIETICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 5718-4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                  APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                             CITY: Charlotte
STATE: No. US20010012886A1th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                       ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
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TELEFAX: 919-881-3175
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APPLICATION NUMBER: US 08/810,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 35 amino acids
TYPE: amino acid
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52.9%;
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Pred. No. 0.0013;
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US-09-776-491-14
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Sequence 14, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                     INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: CUBROWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
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                                                                                                                                                                    TELEFAX: 919-8
TELEX: 575102
                                                                STRANDEDNESS: <Unknown>
                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                           NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Charlotte STATE: No. US20010013135A1th Carolina
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TELEFAX: 919-881-3175
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Pred. No. 0.0016;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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-MODEL-framet_p2n.model -DEV-soft -Q-us-09-720-451-6 -DB=us-09-720-451-5
-SUFFIX=pto -OUT-align6_5 -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0 -UNITS-bits
-START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-1 -DOCALIGN-200
-THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-1 -MODE-LOCAL -OUTFMT-pto
-NORM-ext -HEAPSIZE-500 -MINLENG-0 -MAXLEN-2000000000 -NCPU-6 -NO_XLPXY
-NEG_SCORES-0 -LONGLOG -THREADS-1 -XGAPOD-10 -XGAPEXT-0.1 -FGAPOP-6
-FGAPEXT-0.1 -YGAPOP-10 -YGAPEXT-0.1
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us-09-720-451-5
                                                                             us-09-720-451-6 (1-408) x us-09-720-451-5 (1-558)
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Maximum Match 100%
Listing first I summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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4 IleValThrGlnLeuPheTyrAspThrAspIlePheLeuLysPheValAsnAspCysArg
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Score Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Matches:
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Sea Job	g	ρy	망	QΥ	В	Qy	뭥	Qy	В	Qy	В	Qγ	В	Qγ	В	Qy	B	Qy
rch																		
m co	543	184	483	164	423	144	363	124	303	104	243	84	183	64	123	44	63	24
Search completed: March 4, 2003, 10:53:50 Job time : 1 secs		PheMetArgProArg 188	CCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATTATCAG 542	ProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeuSerAspTyrGln 183	ATCTTTTGGGCAAATCGACAAAAAGCTACATATCAAGGACCATAGGATGGGATCAATAC 482	IlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGlyTrpAspGlnTyr 163	AGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTCC	ArgSerLeuProTrpArgArgProAlaAsnValPheArgValLysGluAspValArgPro 143	GAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTTCT 362	GluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGluSerLysValSer 123	ATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATATG 302	MetCysLyslyslleLeuAlaHisGlyIleLysThrLeuHisLeuTyrThrLeuAsnMet 103	GAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTGAA 242	GluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThrGlu 83	TTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTTTA 182	PheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMetAlaAlaLeu 63	CAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGGGC 122	GlnIleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsnTyrLysGly 43



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Sequence:
                                                                                  Perfect score:
                     Scoring table:
                                                                                                     Title:
                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                             US-09-843-250-33
2408
1 MNYNNKILVSESGLS
                                                                                                                                      January 27, 2003, 08:56:07; Search time 10.1667 Seconds (without alignments) 1299.432 Million cell updates/sec
Gapop 10.0 , Gapext 0.5
                       BLOSUM62
                                                               MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                   GenCore version 5.1.3 Compugen Ltd
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Minimum DB Maximum DB seq length: 0
seq length: 2000000000 Total number of hits satisfying chosen parameters:

262574

262574 seqs, 29422922 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database Issued_Patents_AA:* /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	υ	4	ω	2	. р.		Result No.
94.5	95	96	98	98	99.5	100	101	101	102	102	103	104	106	106.5	106.5	108	108	108	109	110	113.5	168	174	185	223	224		Score
3.9	3.9	4.0	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.4	4.4	4.4	Մ	4.5	4.5	4.5	4.6	4.7	7.0	7.2	7.7	9.3	9.3		Query Match I
350	17	563	5588	5588	256	35	17	17	35	ა 5	35	35	35	649	432	622	35	35	35	35	379	35	ω 5	35	439	446		Length I
2	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	ω	4	4	4	4	4	į	DB
US-08-828-922-1	US-08-810-009-46	US-09-134-001C-4800	US-09-370-700-6	US-09-036-987A-6	US-09-325-932A-57	US-08-810-009-17	US-08-810-009-45	US-08-810-009-44	US-08-810-009-10	US-08-810-009-8	US-08-810-009-11	US-08-810-009-18	US-08-810-009-9	US-08-809-326A-15	US-08-809-326A-16	US-09-311-626B-4	US-08-810-009-15	US-08-810-009-13	US-08-810-009-14	US-08-810-009-12	US-09-028-934-36	US-08-810-009-21	US-08-810-009-20	US-08-810-009-19	US-09-004-393B-2	US-09-004-393B-4		ID
1. N	Sequence 46, Appl	48	6	6, A	57,	17,	45,	44,	10,	8, A	11,	18	9, A	15,	16,	4 , A	15,	13,		12,		21,		19,	Sequence 2, Appli	Sequence 4, Appli		Description

RESULT 2
US-09-004-393B-2
; Sequence 2, Application US/09004393B
; Patent No. 6310771
; GENERAL INFORMATION:

APPLICANT:

Hanson D.,

45	44	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30	29	28
92	92	92	92	92	92	92	92.5	92.5	93	93	93	93	94	94	94	94	1
3. 8	ა 8				3.8											3.9	3.9
1693	1693	1693	1693	1358	1087	1087	525	525	631	631	421	35	1693	1693	1693	560	560
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US-09-402-776-1	US-08-471-971-1	US-08-809-523-1	US-08-840-316-1	US-08-570-311-27	US-08-353-485-8	US-08-570-311-8	US-08-905-817-2	US-08-348-891A-2	US-09-414-453A-12	US-09-345-468-12	US-09-239-303-2	US-08-810-009-16	US-09-553-427-7	US-09-128-275A-7	US-08-478-507-7	US-08-812-829-6	US-08-814-052-6
Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 27, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 2, Appli		Sequence 12, Appl	Sequence 2, Appli	Sequence 16, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 6, Appli	Sequence 6, Appli

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US-09-004-393B-4
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09004393B Patent No. 6310271
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and TITLE OF INVENTION: Plants Transformed Therewith FILE REFERENCE: UF-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rathinasabapathi, Bala APPLICANT: Burnet, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/004,393B CURRENT FILING DATE: 1998-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 446
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Beta vulgaris
275 F-----PMECNWKVFCDNYLDSSYHVPYAH 299
                                        182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                                      216
                                                                                                                            131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMD----YLGDA-----AWYLEPMFKHSGGLE 181
                                                                                                                                                                     159 QGELHAFHNVCTHRA-SILACGSGKKSCFVCPYHGWVYGLDGSLAKA--SKATETQNLDP 215
                                                                                                                                                                                                71 DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                      11 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                                                                                                                                                                                                                                                                                                                   Match 9.3%; Score 224; DB 4; Length 446; Local Similarity 27.4%; Pred. No. 5e-13;
                                                                                   KELGLAPL-KVAEWGPFILISLDRSLDANADVGTEWIGKSAEDVKAHAFDPNLKFTHRSE
                                                                                                                                                                                                                                                             EDALTPPSTWYTEPAFYSHELERIFYKGWQVAGYSEQVKEKNQYFTGSLGNVEYLVSRDG 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08810009 Patent No. 6211437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and TITLE OF INVENTION: Plants Transformed Therewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
CORRESPONDENCES: 65
CORRESPONDENCES: ATTEMPT PARTY OFFICER
                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 NFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 YSHELERIFYKGWQVAGISDQIKEPNQYFTGSLGNVEYLVSRDGEGKVHAFHNVCTHRA- 166
                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Dra
CITY: Charlotte
STATE: No. 62114
TELEPHONE: 919-881-3175
                                                                          REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 04-MAR
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYLDSSYHVPYAH 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SILACGSGKKSCFVCPYHGWVYGMDGSLAKASKAKP--EQNLDPKELGLVPL-KVAVWGP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
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                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                            US/08/810,009
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                                                                            5718-4
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Pred. No. 6e-13;
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Patent No.
                                                               Matches
                                                                               Query Match
Best Local S
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Best Local Similarity 94.3%;
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                                                                                                                                                                                                                                               TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Briggs, Ste
APPLICANT: Johal, Gurn
APPLICANT: Gray, John
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                               y Match 7.2%;
Local Similarity 85.7%;
hes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
                 79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
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5. 6211437
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                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                              35 amino acids
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                                                                                                                                                                 linear
                                                                                                                                              protein
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, Gurmukh S.
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Pred. No. 5.4e-11;
                                                                               Score 174; DB 4;
Pred. No. 6.1e-10,
                                                                 Mismatches
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                                                                                              Length 35
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RESULT 5 US-08-810-009-21

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US-09-028-934-36
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                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/09028934 Patent No. 6117670
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Best Local 9
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ligon,
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APPLICANT: Briggs
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TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/810,009

FILTING DATE:
                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
                                                                                                                                        APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                                                                                                                                                                                                                  APPLICANT:
                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                       NUMBER OF SEQUENCES:
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COUNTRY: US
ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Spruill, W. Murray REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                 CITY: Research Triangle Park
STATE: NC
                                                                    STREET:
                                                                      ADDRESSEE: No. 6117670artis Corporation STREET: 3054 Cornwallis Road
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No. 6211437th Carolina
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Hill, Dwight :
Lam, Steven T
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van Pee, Karl-Heinz
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80.0%;
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Pred. No. 2.3e-09;
3; Mismatches 4
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US-08-810-009-12

Sequence 12, Application US/08810009

Patent No. 6211437

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.
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                                                                                                 RESULT 7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNBY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                        333
                                                                                                                                                                                       372 NGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSN 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PVVMERYCSHLGASL-----AKGKVVEGCIQCPFHNWRYDSTGACSHVP-----GHS 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 01 FILING DATE: 09-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/028,934 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 IHGDEELFQ-----HELKTIFARNW-LFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGS 73
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les 96; Conserv
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                                                                                                                                                      GGGAFSKYDQLIL----
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                                                                                                                                                                                                                                                                                                                                                                          PPPGQEALARDGAWFGAGIDFHVDRYFGPLGVISRTLGLSMSRMQLHFDGYPG-----
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                                                                                                                                                                                                                                                                                                   -----GCIMTVSLD---GDVKYRL----LQCV------
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                                                                                                                                                                                                                               -GDGVVRSAANFILYGLQTWAAAGYDVAIWNSMKAD
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US-08-810-009-14
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Best Local Similarity 52.9
"""ches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION: 919-881-3140
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ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
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MEDIUM TYPE: Floppy disk
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APPLICANT: Gray, John
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                                                                                                                                                                                             STREET: P.O. Dra
APPLICATION NUMBER: US/0 FILING DATE: 04-MAR-1997
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Charlotte
STATE: No. 6211437th Carolina
                                                                                                                                                               COUNTRY:
                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
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                                                                                                                                                                                                                    P.O. Drawer 34009
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                                                                                                                                                                                  6211437th Carolina
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52.9%;
                US/08/810,009
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Pred. No. 0.00079;
                                                      Version #1.30
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US-08-810-009-13
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US-08-810-009-13
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TELEX: 575102
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
FRNGTH: 35 amino acids
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Best Local Similarity 52.9%;
Matches 18; Conservative
                                                                                                                                                                      TELEFAX: 919-881-31/5
TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5716
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65 '
                                                                                                                                            SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    TELEPHONE: 919-00-
                                                                                                                                                                                                                                                                                                                                           FILING DATE: 0. CLASSIFICATION:
                                                                                       TOPOLOGY:
                                                                                                      STRANDEDNESS:
                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte
STATE: No. 6211437th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NQCRHRGMRICRADGGNAKSPTCSYHGWAYDSAG 34
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                                                                                                                           amino acid
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                                                                     protein
4.5%;
52.9%;
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Pred. No. 0.00098;
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Score 108; DB 4; Pred. No. 0.0012;
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              Length 35;
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Query Match Best Local Similarity

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                                                                                                             GENERAL INFORMATION:
                                                                                                                        Sequence 4, Application US/09311626B Patent No. 6399347
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Patent No.
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Best Local
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                                                   APPLICANT: Jorgensen,
APPLICANT: Schnorr, F
APPLICANT: Andersen,
APPLICANT: Schulein,
        APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
 CURRENT APPLICATION NUMBER: US/09/311,626B
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 04-MAR-199
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1i MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Johal, Guri
APPLICANT: Gray, John
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NAME: Spruill, W. Murray
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                                                                                                                                                                                                                                                                                                                                                           LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
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STATE:
                                                                                                                                                                                                                                                                             Local Similarity
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                                                  Andersen, Lene No. 6399347boe
Schulein, Martin
                                                                                 Schnorr, Kirk
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N: 800
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                                                                                                                                                                                                                                                                          Score 108; DB 4; Length 35; Pred. No. 0.0012;
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TYPE: PRT
COMPUTER READABLE FORM:
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            COUNTRY: USA
ZIP: 10036-2711
                                      STATE:
                                                                STREET:
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US-08-809-326A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Izutsu
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PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: 60/084,
PRIOR FILING DATE: 1998-05-05
                                                                                                                                   TITLE OF INVENTION:
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APPLICANT:
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                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 ----NKEIG-DVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTT-EVWTYAIVE
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                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 RGKTLVSVEAG--NAKGFVCS------YHGWGFGSNGELQSVPFEK-------DLYG
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New York
                                                         1155 Avenue
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Matsumoto, Akira
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                                                                                     Pennie &
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                                                                                                                                                                                                                        CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, NETHORS CONTAINING THE POLYPEPTIDES, DNAS CODING FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING THEREEOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF ANTIBODY, METHOD AND REAGENTS FOR DEFECTION AND/OR MEASUREM OF ANTIBODY, METHOD AND AGENTS FOR DEFECTION AND PROBES AND PRIMERS FOR DEFECTION AND MEASUREMENT OF CHLAMYDIA PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DEFECTION AND MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
                                                                                                                                                                          PNEUMONIAE GENE
                                                                                                                                                                                                         REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                         of
                                                                                  Edmonds LLP
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                                                                                        RESULT 13
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                Sequence 15, Application US/08809326A Patent No. 6165478 GENERAL INFORMATION:
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Best Local (
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FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                        67 GTDDRVTW-----VKSVDEAIAACGDVPEIMVIGGG---RVYEQFLPKAQKLYLTHIDAE 118
                                                                                                                                                                                                                                                                                                                                                                                                                              22 WNLPAD-----LAWFKRNTLNKPVIMGRHTWESIGRPLPGR------KNIILSSQP 66
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53; Conserv
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amino acid
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Izutsu, Hiroshi
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SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,
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APPLICATION NUMBER:
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247 GSGMGVLWDGYSGVHSADL------VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
                                                                                           195 WKAPAENFVGDAYHVGWTHASSL------RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
                                                         22 WNLPAD------LAWFKRNTLNKPVIMGRHTWESIGRPLPGR-----KNIILSSQP 66
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                                                                                                                                Conservative
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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21.4%;
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FIGSED PROTEINS CONTAINING THE POLYPEPTIDES, DAAS CODING
FIGSED PROTEINS CONTAINING THE POLYPEPTIDES, TRANSFORMA
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSTS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNEUMONIAE GENE
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                                                                                                                                                   Score 106.5; D
Pred. No. 0.15;
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                                                                                                                                Mismatches
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                                                                                                                                                                  Length
                                                                                                                                                                    649;
                                                                                                                                67;
                                                                                                                              Gaps
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RESULT 15

US-08-810-009-18

; Sequence 18, Application US/08810009

; Patent No. 6211437

; GENERAL INFORMATION:
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Best Local Similarity 51.4
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CIASTITICATION. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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STATE: N
COUNTRY:
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STRANDEDNESS:
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Pred. No. 0.0019;
4; Mismatches 13
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Search completed: January 27, 2003, 09:04:54 Job time: 11.1667 secs

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-810-009-18
                                                                             Matches
                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #10, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Charlotte cmame: No. 6211437th Carolina
                                     79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                         Local Similarity 52.9 nes 18; Conservative
                                                                                                                                                                                                          STRANDEDNESS:
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TELEFAX: 919-881-3175
TELEX: 575102
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1 NSCRHRGALLCPFSKGNQKFHVCRYHGWSYDSSG
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P.O. Drawer 34009
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Johal, Gurmukh S.
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                                                                                             4.3%;
52.9%;
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                                                                                           Score 104; DB 4
Pred. No. 0.003;
                                                                           Mismatches
 34
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 08:54:32; Search time 25.8333 Seconds
(without alignments)
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Scoring table: BLOSUM62 Gapop 10	Title: Perfect score: Sequence:	
BLOSUM62 Gapop 10.0 , Gapext 0.5	US-09-843-250-33 2408 1 MNYNNKILVSESGLSQKHLIAEFEHASSTWHTELTKTTDR 449	3581.232 Million cell updates/sec

Total number of hits satisfying chosen parameters: 671580

671580 seqs, 206047115 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_nwann:*
6: sp_mammal:*
7: sp_mhc:*
1: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_archeap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14) L	12	11	10	9	8	7	6	. СП	4	ω	2	-	NO.	Result
1405	1451	1483	1484	1486	1488	1490	1968.5	2022	2051	2071	2187	2191	2206	2290	2330	score)
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Q9EUC7	Q9F5S3	Q9F5S9	Q9F5S8	Q9F5T3	Q9F5S4	Q9ETK2	Q45695	Q8RTL4	P95564	Q8VUD4	052382	Q9L5D2	Q9ZI73	Q52142	Q938R9	ID	1
Q9euc7 pseudomonas	Q9f5s3 pseudomonas	Q9f5s9 pseudomonas	Q9f5s8 pseudomonas	Q9f5t3 pseudomonas	Q9f5s4 pseudomonas	Q9etk2 pseudomonas	Q45695 burkholderi	Q8rt14 comamonas s	P95564 pseudomonas	Q8vud4 burkholderi	052382 ralstonia s	Q915d2 comamonas t	Q9zi73 pseudomonas	' Q52142 pseudomonas	Q938r9 pseudomonas	Description	

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	٠ د		_	Q8vum2 ralstonia	Q8vr21 burkh	Q8vum5 napth	-					Q8vr24 pseud	_		Q8vum6 ralst	w	\sim		01	Q9f5t0 pseud				7					
ancarcarea	turod	uncultured	uncultured	onia s	burkholderi	napthalene	marinobacte	alcaligenes	burkholderi	burkholderi	pseudomonas	pseudomonas	pseudomonas	pseudomonas	ralstonia s	burkholderi	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas	pseudomonas

ALIGNMENTS

Qy	Qу	Qy	Qu Ma	SQ	DR	DR DR	DR	DR :	D A	RA	RP	g C	28	8	SO	GN	DE	DΤ	DΤ	ဌ	AC	ID	Q938R9	RESULT	
121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 	1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60 	Query Match 96.8%; Score 2330; DB 2; Length 449; Best Local Similarity 96.0%; Pred. No. 6.1e-171; Matches 431; Conservative 12; Mismatches 6; Indels 0; Gaps	DIOXYGENBE. SEQUENCE 449 AA; 49608 MW; 5EFEDBE0282FE812 CRC64;	E; PS0057	Pfam; PF00355; Rieske; l. Pfam; PF00848; Ring_hydroxyl_A; l.	Pro; IPR001663;	InterPro; IPR001281; Rieske.	SUDMITTER (OCT-2001) TO THE EMBL/SERBARK/DDBJ GATADASES.	1.7	SEQUENCE FROM N.A.	NCB1_Tax1D=294;	Pseudomonas.		Pseudomonas fluorescens.		dioxygenase.	(TrembLrel. 20, Last annotation	(TrEMBLrel. 19,	(TrEMBLrel.	Q938R9;	Q938R9 PRELIMINARY; PRT; 449 AA.	BR9	Tr. or 1	

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Query Match
Best Local Similarity
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Q52142; 008194;
Q1-NOV-1996 (TrE
01-NOV-1996 (TrE
01-DEC-2001 (TrE
Iron-sulfer prot
PAHAC.
                                                                                                                                         "The molecular analysis of NAH7-type of chromosomes of Pseudomonas aeruginosa OUS82.",
Submitted (JUN-1997) to the EMBL/GenBa
                                                                                                                                                                                                                                                    "Identification and characterization of genes encoding po
aromatic hydrocarbon dioxygenase and polycyclic aromatic
dihydrodiol dehydrogenase in Pseudomonas putida OUS82.";
J. Bacteriol. 176:2444-2449(1994).
                                                                                                                                                                                                                                                                                                            STRAIN-OUS82; STRAIN-OUS82; PubMed-8157615; MEDLINE-94209249; PubMed-8157615; Vaida N., Torigoe S.,
                                  Pfam: PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASC
PROSTITE: PS00570; RING_HYDROXXL_ALPHA; 1.
SEQUENCE 449 AA; 49361 MW; 80020F54AAB11E8A
                                                                                             InterPro;
InterPro;
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Bacteria; Proteobacteria;
                                                                                                                                 EMBL;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                         Noboru T., Toshiya I., Takashi S., Kazuhiro
Yue-Wu W., Masao F., Hohzoh K.;
                                                                                                                                                                                                                  STRAIN=OUS82
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Pro: IPR001281; Rieske.
Pro: IPR001663; Ring_hydroxyl_A.
PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
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                                                                                                                                 AB004059; BAA20391.1;
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(TremBLrel. 01, Last sequence up
(TremBLrel. 19, Last annotation
protein large subunit.
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95.1%;
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Score 2290; DB 2; Pred. No. 7.3e-168;
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Q9ZI73;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                        Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99365311; PubMed=10433976;
Bosch R., Garcia-Valdes E., Moore E.R.B.;
"Genetic characterization and evolutionary implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas stutzeri (Pseu
Bacteria; Proteobacteria;
                                                                                                                                     Dioxygenase
SEQUENCE '
                                                                                                                                                                                                                                                                   InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                        EMBL; AF039533; AAD02136.1; HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas stutzeri AN10.";
Gene 236:149-157(1999).
                                                                                                                                                                                                                                                                                                                                                                       Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=316;
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NAHAC.
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                                                                  Similarity
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dioxygenase Fe-S large subunit.
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                                                                                                                                                                                  RING_HYDROXYL_ALPHA;
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89.5%;
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eria; gamma subdivision; Pseu
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                                             Score 2206; D
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25; Mismatches
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                                             DB 2;
1e-161;
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PKELLILL
Q9L5D2;
Q9L5D2;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                Appl. Microbiol. Biotechnol. 55:609-618(2001).
EMBL; APE25250; AAF72976.1; -.
HSSP; P23094; 1NDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                 Dioxygenase.
SEQUENCE 4
                                                                                                                                                                                                                                                                      Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00190; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Insights into the genetic diversity of initial degrading bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moser R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21306905; PubMed=11414329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=285;
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  IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                    MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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                                                              MIYEN--LVSEAGLTQKHLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVTAKMG 58
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                                                                                                                                                   399;
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                        PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stahl
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88.9%;
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ia; beta subdivision; Comamonadaceae;
                                                                                                                                                 27;
                                                                                                                                            Score 2191; DB 2;
Pred. No. 3e-160;
7; Mismatches 21;
                                                                                                                                                                                                                               2950EF36123A6F21 CRC64;
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Query Match
Best Local Similarity
Matches 400; Conserv
                                                                                                                                    InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
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01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
Naphthalene 1,2 dioxygenase
                                                                                                                                                                                                                                                                                                                                    Zhou N.Y., Fuenmayor S.L., Williams P.A.;
"nag genes of ralstonia (Formerly pseudomonas)
enzymes for gentisate catabolism.";
J. Bacteriol. 183:700-708(2001).
                                                                                              Dioxygenase; Plasmid
SEQUENCE 447 AA;
                                                                                                                                                                                                                                                                                    EMBL; AF036940; AAD12610.1; HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fuenmayor S.L., Wild M., Boyes A.L., Williams "A gene cluster encoding steps in conversion c gentisate in Pseudomonas sp. strain U2."; J. Bacteriol. 180:2522-2530(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98233751; PubMed=9573207;
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
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                        90.8%;
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large oxygenase compo
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Score 2187; DB 2;
Pred. No. 6.1e-160;
5; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                              4553AAF4B4410ED0 CRC64;
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                                               Length
    Indels
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Matches 375
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01-MAR-2002
01-MAR-2002
01-JUN-2002
DntAC.
                                                                                                               Piam; PF00355; Rieske; 1.

Pfam; PF00848; Ring_hydroxyl_A; 1.

PRINTS; PR0099; RNGDIOXCNASE.

PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.

PROSITE; PS00570; A 49468 MW; 2A5BF8558320275C CRC64;
                                                                                                                                                                                                                                                    Johnson G.R., Jain R.K., Spain J.C.;
"Origins of the 2,4-dinitrotoluene pathway.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF169302; AAL50021.1;
InterPro; IPR001281; Rieske.
InterPro; IPR00163; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20254695; PubMed-10795678; Johnson G.R., Jain R.K., Spain J.C.; "Properties of the trihydroxytoluene oxygenase cepacia R34: an extradiol dioxygenase from the pathway."; Arch. Microbiol. 173:86-90(2000).
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                                              al Similarity
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Last sequence up
                                         Score 2071; DB 2;
Pred. No. 5.1e-151;
8; Mismatches 34;
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                                                                                                                                                                                               Query Match
Best Local Sin
Matches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parales J.V., Kumar A., Parales R.E., Gibson I "Cloning and sequencing of the genes encoding dioxygenase from Pseudomonas sp. JS42."; Gene 181:57-61(1996).
EMBL; U49504; AAB40383.1; -.
                                                                                                                                                                                                                                                                                          Interpro; IPRO01281; Rieske.
Interpro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSTTE; P800570; RING_HYDROXYL_ALPHA; 1.
SEQUENCE 447 AA; 49485 MW; ICB0E223E5
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Bacteria; Proteobacteria.
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83.7%;
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Pred. No. 1.7e
34; Mismatches
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Lessner D.J., Johnson G.R., Parales R.E., Spain J.C.,
"Molecular Characterization and Substrate Specificity
Dioxygenase from Comamonas sp. Strain JS765.";
Appl. Environ. Microbiol. 68:634-641(2002).
EMBL, AF379638; ARJ/6202.1; -
SEQUENCE 447 AA; 49556 MW; 4CA961F99A37DF3A CRC64;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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QMTSKYGSGMGVFWGYYSGNFSADMIPDLMAFGAAKQEKLAKEIGDVRARIYRSFLNGTI
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Proteobacteria;
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40; Mismatches
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01-NOV-1996
01-DEC-2001
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EMBL; U62430;
HSSP; P23094;
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Q45695;
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PRINTS; PRO0090; RING_HYDROXYL_ALPHA; 1.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
4827 MW; 726736C29CEF9A10 CRC64;
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity to naphthalene dioxygenase. J. Bacteriol. 178:4926-4934(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia sp. (strain |
Bacteria; Proteobacteria;
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DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                 FPNNCFLTGAGVFKVFNPIDENTTEAWTYAIVEKDMPEDLKRRLADAAQRSTGPAGYWES
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Matches 277
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Q9ETK2;
01-MAR-2001
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Q9F5S4;
01-MAR-2001
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Naphthalene dioxygenase
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InterPro; IPR001663; Ring_hydroxyl_A.
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Bacteria; Proteobacteria;
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ilarity 100.0%;
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sulfur protein 2 (Fragment).
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Reference M.A., Lalucat J., Bosch R.;

"Coexistence of two naphthalene dioxygenase genes (napseudomonas strains from West Mediterranean Sea.";

Esubmitted (SEP-2000) to the EMBL/GenBank/DDBJ databas EMBL, AF306440, AAC25700.1;

REMBL, AF306440, AAC25700.1;

RISEP, P23094; INDO

InterPro; IPR001281; Rieske.

InterPro; IPR001281; Rieske.

InterPro; IPR001563; Ring_hydroxyl_A.

Pfam; PF00355; Rieske; 1.

PFAMTTS; PR00390; RNGDIOXNASE.

PRAINTS; PR00090; RNGDIOXNASE.
"Coexistence of two naphthalesch R.; "Coexistence of two naphthalesch dioxygenase genes Pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ data
                                                                 STRAIN-19IIDNH;
                                                                                                                                                                  Pseudomonas sp.
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                                                                                                                NCBI_TaxID=139738;
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NCBI_TaxID=303;
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76; Conservative
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277 AA;
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(TIEMBLrel. 16, Last sequence update)
(TIEMBLrel. 19, Last annotation update)
dioxygenase iron sulfur protein (Frag
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AF306426; AAG25686.1; P23094; INDO.

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RESULT 13
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Best Local :
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                                 NON_TER
NON_TER
SEQUENCE
                                                                                                                 Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase genes (nahAc)
"seudomonas strains from West Mediterranean Sea.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF306434; AA625694.1; -.
HSSP; P23094; 1NDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                   Dioxygenase.
                                                                               PROSITE;
                                                                                      Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                   STRAIN-PR3MN2;
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Bacteria; Proteobacteria;
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01-MAR-2001 (TrEMBLrel.
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01-DEC-did tremblarel.
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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Score 1484;
Pred. No. 3
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Pred. No. 2.4e-106;
D; Mismatches 1;
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34; DB 2;
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RESULT 14
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Best Local Sin
Matches 276;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrero M.A., Lalucat J., Bosch R.; "Coexistence of two naphthalene dioxygenase genes (nahAc) Pseudomonas strains from West Mediterranean Sea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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NCBI_TaxID=139736;
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EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH
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29995 MW;
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Pred. No. 4.2e
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Best Local Similarity 96.8%;
Matches 268; Conservative
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Coexistence of two naphthalene dioxygenase genes (nahAc) Beeudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF306441; AAQZ5701.1; -. HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9F553;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein 1 (Fragment).
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Pfam; PF00848; Ring_hydroxyl_A; 1.

PRLWTS; PR00909; RRODIOXOMASE.

PROSITE; PS00570; RING_HYDROXYL_ALI
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InterPro; IPR001663; Ring_hydroxyl_A.
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Bacteria; Proteobacteria;
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                                                                                                                                     HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP 235
                                                                                                                                                                                 SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                                                                                                                                              TAKMGIDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQ 60
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277 AA;
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; 30062 MW;
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          2003, 09:02:20
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us-09-843-250-33.rsp

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 08:47:32; Search time 7.16667 Seconds (without alignments) 2598.540 Million cell updates/sec

Title: Perfect score:

US-09-843-250-33
2408
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
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ALIGNMENTS

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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. [6]	alene metabolism of NPL1 plasmid f	sequences of genes encoding an upper pathway of	TRAIN=BS202; PLASMID=	[5]	e 127:31-37(1993	ncoding naphthalene dioxygenase	Suen WC., Cruden D.L., Gibson D.T., Zyl	nd T.D., Saunders R., Ensley B.D.	<pre>MEDLINE=93252277; PubMed=8486285;</pre>			J. Bacteriol. 175:6890-6901(1993).	complete DNA sequence of an upper naphthal		226631;		SEQUENCE FROM N.A.	(**** #///) *** **** #****/ *****/ *****/ *****/	Parales J.V., Parales R.E., Kumar A., Gibson D.T.; Submitted (MAR-1996) to the FMBL/GenBank/DDRJ databases	putida; STRAIN=NCIB 9816;	SEQUENCE FROM N.A.	(2)	of Pseudomonas putida strain NCIB98	, nucleotide sequence and characteriza	Kurkela S., Lehvaeslaiho H., Palva E.T., Teeri T.H.;	SPECIES=P.putlda; STRAIN=NCIB 9816; MEDLINE=89211973: PubMed=3243438:	SEQUENCE FROM N.A.		VCBT TAYID=303 306.	oteobacteria; gamma subdivis	31, Plasmid NAH7, and	_	NDOB OR NAHAC OR DOXB OR NAHA3 OR NDOC2.	nase ISP alpha).	(Rel. 41, Last annotation update)	(Rel. 20, Last	P23094; Q52124; O33461; O07830; O1-NOV-1991 (Rel. 20, Created)	NDOB_PSEPU ID NDOB_PSEPU STANDARD; PRT; 449 AA.	[TT]

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EMBL; M23914; AAB47591.1; -. EMBL; U49496; AAA92141.1; -. EMBL; M60405; AAA16125.1; -. EMBL; M83949; AAA25902.1; -. EMBL; AF010471; AAB62707.1; -. EMBL; AF0104284; AAB61373.1; -.
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Pfam; PF00848; Ring_hydroxyl_A; 1.

PRINTS; PR00090; RNGDIOXGNASE.

PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
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Interpro; IPR001281; Rieske.
Interpro; IPR001663; Ring_hydroxyl_A.
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Structure 6:571-586(1998)
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Ramaswamy S.
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MEDLINE-98298434; PubMed-9634695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1, dihydronaphthalene-1,2-diol + NAD(+).

COEACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHIOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTH-1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DBT IS LIVOXIDATION OF THE AROMATIC RING.

SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENSY SUBUNITE NAPHTHALENE DIOXYGENE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT AND AN IRON SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN (RUDCH) AND FERREDOXIN (RUDCH), AND ISP ISS COMPOSED OF AN HEXAMER OF THREE LARGE ALPHA SUBUNITS (NDOB) AND THREE SMALL BETA SUBUNITS (NDOC).

SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CISNAPHTHALENE DIHYDRODIOL.
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B49343; B49343.
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15-DEC-1998
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NDOB OR NDOC2.
                                                                                                                    Plasmid
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
1,2-dioxygenase alpha subunit (EC
                                                                                                                              fluorescens
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ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF004283; AAB61370.1; HSSP; P23094; 1NDO.
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COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES

CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF

DIBENZOTHIOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHREN

1-HYDROXY-2-NAPTHOIC AND THE METABOLISM OF DBT IS LIMITE

OXIDATION OF THE AROMATIC RING.

SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME

SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
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                DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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NAPHTHALENE DIHYDRODIOL.

1- CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1,2-
dihydronaphthalene-1,2-diol + NAD(+).

1- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

1- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

1- PATHAY: UPDER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES
CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF
DIBENZOTHIOPHENE (DET) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO
1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DET IS LIMITED TO
OXLDATION OF THE AROMATIC RING.

1- SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT AND AN IRON
SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED
OF FERREDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS

COMPOSED OF A LARGE ALPHA SUBUNIT (NDOB) AND A SMALL BETA SUBUNIT
                                                                                                                                                                                                        Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION
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15-JUN-2002 (Rel. 41, Last annotat
Naphthalene 1,2-dioxygenase alpha
1,2-dioxygenase ISP alpha).
                                                                                                                                                                                                                                                                                                               EMBL; D84146; BAA12240.1; -. HSSP; P23094; INDO. InterPro; IPR001281; Rieske.
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15-DEC-1998 (Rel.
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Kiyohara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                     PROSITE;
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41, Last annotation updat
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IRON-SULFUR (2FE-2S)
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IRON (BY SIMILARITY).
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Matches 403
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                                                                SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R.
Gregor J., Davis N.W., Kirkpatrick H.A., Gov
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METAL
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Turlin E.,
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                                                      B., Shao Y.;
                          complete genome sequence complete genome sequence 277:1453-1474(1997).
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Pred. No. 6.7e-167;
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                                        coli K-12
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EMBL; 237966; CAA86018.1; --
EMBL; AE000340; AAC75591.1; --
EMBL; AE000340; BAA16433.1; --
EMBL; D90883; BAA16441.1; --
EMBL; AE005484; BAA1657651.1; --
EMBL; AE002562; BAB36827.1; --
HSSP; P23094; INDO.
ECOGene; EG13456; hcaE.
 Aromatic hydrocarbons of Dioxygenase; NAD; Complemental 85 85 METAL 87 87 METAL 105 105
Dioxygenase;
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                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Welch R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuha
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasund
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K.,
Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700 MEDLINE=21074935; PubMed=11206551;
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                                                             PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                         InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                     PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
S; PR00090; RNGDIOXGNASE.
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 Complete
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                                                  Iron-sulfur; Iron;
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Best Local S
Matches 165
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01-NOV-1995 (Rel. 32, Cre
01-NOV-1995 (Rel. 32, Las
16-OCT-2001 (Rel. 40, Las
Benzene 1,2-dioxygenase a
                                                                                                                                                                                                                                                                                                          _PSEPU
                                                MEDLINE=93345820; PubMed=8344526;
Tan H.-M., Tang H.-Y., Joannou C., Abdel-Wahab N.H., Mason
"The Pseudomonas putida ML2 plasmid-encoded genes for benze
dioxygenase are unusual in codon usage and low in G+C conte
Gene 130:33-39(1993).
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CONFLICT
CONFLICT
     <del>-</del> - <del>-</del> -
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                                                                                                               STRAIN-ML2;
                                                                                                                                                      NCBI_TaxID=303;
                                                                                                                                                                                                      Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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CATALYTIC ACTIVITY: Benzene + NADH + O(2) = dihydrobenzene-1,2-diol + NAD(+).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND PATHWAY: FIRST STEP OF DEGRADATION OF BENZEN
                                                                                                                                                                                                                                                                                                                                                       ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTA
                                                                                                                                                                                                                                                                                                                                                                                YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK
                                                                                                                                                                                                                                                                                                                                                                                                        GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA 420
                                                                                                                                                                                                                                                                                                                                                                                                                               GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVESYKGLIFGNWDTSAPGLRDYLGDIAWYLDGMLDRREGGTEIVGGVQKWVINCNWKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AENFVGDAYHVGWTHASSL-------RSGESIFSSLAGNAALP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCRHRAMRVSYADCGNTRAFTCPYHGWSYGINGELIDVPLEPRAYPQGLCKSHWGLNEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYTDPDIYQLELERIFGRCWLFLAHESQIPKPGDFFNTYMGEDAVVVVRQKDGSIKAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165; Conserv
                                                                                                                                                                                        рнмт112
                                                                                                                             FROM N.A.,
                                                                                                                                                                           Proteobacteria;
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213
218
218
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384
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                                                                                                                            SEQUENCE
                                                                                                                                                                                                                              alpha
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                                                                                                                                                                             gamma
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IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
V -> A (IN REF. 1).
GHRARNSKLCLEMGLGGEKRADDGIPGITNVIFSETAARGM YQRWADLLSSEWGEVLDKTAAYQQEVMK -> ATAPATAN CVWKWGLVRKSAATTAFLALLTISFQKLPLVECTNAGPIF
                                                                                                                                                                                                                               subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN REF. 1)
                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                             subdivision;
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                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                             update)
(EC 1.14.12.3).
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  BENZENE
                                                                                                                                                                             Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GQTARPVWETAKDALQFG
              AN IRON ATOM
                                     cis-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 453;
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  TO
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                                                                content.";
                                                                          benzene
                                                                                      J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00090; RNGDIOXGNASE PROSITE; PS00570; RING_HYDROX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF148496; AAA17758.1; HSSP; P23094; INDO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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InterPro; IPR001663; Ring_hydroxyl_A.
                                                            436
                                                                                                                     376
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SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BEDC1 AND BEDC2)
                                                            KMMTSPDW
                                                                                         AHVSSSNW
                                                                                                                                                 DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ 421
                                                                                                                                                                                                                                        WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF
                                                                                                                                                                                                                                                                     WDGY-SGVHSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                     VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                    DGENWVEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
                                                                                                                                                                                                          PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWESD
                                                                                                                                                                                                                                                                                                 WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP-----KFGKQYRAS
                                                                                                                                                                                                                                                                                                                    WKAPAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
                                                                                                                                                                                                                                                                                                                                                            PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
                                                                                                                                                                                                                                                                                                                                                                                        --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                                                                                                                                                                                                                                                                     QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA-----CLDKKEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYTDEDLYQLELERVFARSWLLLGHETHIRKPGDYFTTYMGEDPVVVVRQKDASIAVFLN
                                                                                                                                                                               PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
148; Conserv
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96
98
116
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222
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228
450 AF
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                                                                                         429
                                                            443
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                                                                                                                                                                                                                                                                    -----LVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid.
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98 II
116 II
119 II
222 II
228 II
2108 MW;
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IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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(BY SIMILARITY).
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450;
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Matches 145
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HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF000848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990
01-JAN-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                METAL
SEQUENCE
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Toluene degradation by Pseudomonas putida F1. Nucleotide the todC1C2BADE genes and their expression in Escherichia J. Biol. Chem. 264:14940-14946(1989).
-:- COFACTOR: PROBABLY BINDS A ZFE-ZS GROUP AND AN IRON A -:- PATHWAY: Toluene degradation; first step.
-:- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTWO SUBUNITS OF THE HYDROXYLASE COMPONENT (TODC1 AND
                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                         Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                             METAI
                                                                                                                                                                                                                                                                                                                                                                                   Aromatic hydrocarbons catabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04996; AAA26005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zylstra G.J., Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89359301; PubMed=2670929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                         209
 252
                                                                            149
                                                                                                    138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERREDOXIN (TODB) AND A FERREDOXIN REDUCTASE (TODA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no resti
VLWDGYSGVHSADLVPELMAF---GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                                                                                        --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                          VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE---
                                                                                                                                                                           IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
                         WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----
                                                  WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                          PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                                                          QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                                                                                                                145;
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(Rel. 13, Last seq
(Rel. 41, Last ann
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ast annotation update)
alpha subunit (EC 1.14.12.-).
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                                                                                                                                                                                                                                                                                 MW;
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Pred. No. 1.5e
71; Mismatches
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IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase;
                                                                                                                                                                                                                                           No. 1.
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                                                                                                                                                                                                                              .5e-43;
les 181;
                                                                                                                                                                                                                                                                                                                                             (2FE-2S)
(2FE-2S)
                          EMADLAPPTVGKQYRASWGGHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as its content
                                                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                                 CRC64;
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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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use by non-profit institutions as long modified and this statement is not removed.

requires a license agreement (S an email to license@isb-sib.ch).

(See

http://www.isb-sib.ch/announce,

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                                                                                                                                                                                                                                   Haddock J.D., Gibson D.T.,
J. Bacteriol. 178:2158-2158(1996).
J. Bacteriol. 178:2158-2158(1996).
J. CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) =
phenylcyclohexa-3,5-diene-1,2-dio1 + NAD(+).
J. COFACTOR: Binds 1 2Fe-2S cluster and 1 iron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BURCE
                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequencing and transcriptional mapping encoding biphenyl dioxygenase, a multicomponent polychlorinated-biphenyl-degrading enzyme in Pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dioxygenase)
                                                                                                     between
                                                                                                                                                                                                                                                                                                                               "Purification and characterization of the oxygenase component of biphenyl 2,3-dioxygenase from Pseudomonas sp. strain LB400."; J. Bacteriol. 177:5834-5839(1995).
                                                                                                                                                                                                                                                                                                                                           biphenyl
                                                                                                                                                                                                                                                                                                                                                                      Haddock J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-LB400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biphenyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994
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                                                                                                                                                                                                                                                                                                       ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96011369; PubMed=7592331;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LB400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92234948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last sequence up. 15-JUN-2002 (Rel. 41, Last annotation Biphenyl dioxygenase alpha subunit (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 174:2903-2912(1992)
                                                                                      s SWISS-PROT entry is copyright. It is produced through
ween the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no rest
                                                                                                                                       SUBUNIT: Heterohexamer consisting of three BphA subunit BphE subunits. A ferredoxin (BphF) and a ferredoxin red (BphG) must be present to obtain activity.

SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                       PATHWAY: Biphenyl-polychlorinated biphenyl
                                                                                                                                                                                                            first step
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1569021;
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eria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                             NADH + O(2) = (2R, 3S) - 3
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C 1.14.12.
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degradation pathwa
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                                                                                                                                                                                   reductase
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L outstation -
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BPHA_COMTE
ID BPHA_CA
AC Q46372
AC Q46372
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 61000
DE Biphen
DE dioxyg
GN BPHA.
OS COMBANO
OC Bacter
OX NCBI_T
RN [1]
RN [1]
RP SEQUEN
RC STRAIM
RX MEDLIM
RA Sylves
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Best Local Similarity
                                                                                                                                 BPHA_COMTE STAN
Q46372;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUN-2002 (Rel. 4
 MEDLINE=97045812;
Sylvestre M., Sire
                                                                           Comamonas
Bacteria;
                                                                                                            dioxygenase).
                                                                                                                     Biphenyl dioxygenase
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SEQUENCE
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METAL
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INIT_MET
                            STRAIN-B-356;
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                                      SEQUENCE FROM
                                                              NCBI_TaxID=285;
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PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMGIDEVIVSRQN 70
                                                                                                                                                                                                                                                                                                                     SYQRTAGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDYYGDAYYPGVYGKS 406
                                                                                                                                                                                                                                                                                                                                                            VRARIIRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                                                                                                                                                             QIPTK-GNQFRAAWGGHGSGWYVDEPGSLLAVMGPKVTQYWTEGPAAELAEQRLGHTGMP
                                                                                                                                                                                                                                                                                                                                                                                                                       QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCLGLKEV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKSIKVFLNQCRHRGMRICRSDAGNAKAFTCSYHGWAYDIAGKLVNVPFEKEAFCDKKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKGLLDPR-IYADQSLYELELERVFGRSWLLLGHESHVPETGDFLATYMGEDPVVMVRQK 88
                                                                                                                                                                                                                                                                      AIGETSYRGFYRAYQAHVSSSNWA
                                                                                                                                                                                                                                                                                               HNIRNFSAGGVFEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y
                                                                                                                                                                                                                                                                                                                                              VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGMQKWVIPCNWKFAAEQFCSDMYHAGTTTHLSGILAG-----IPPEMDLSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DC-GFDKAEWGPLQARVATYKGLVFANWDVQAPDLETYLGDARPYMDVMLDRTPAGTVAI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146;
                                                                        Proteobacteria;
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458 2
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   Sirois
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51382
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              PubMed=8890734;
                                                                                                                      , Last sequence update)
, Last annotation update)
alpha subunit (EC 1.14.12
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32.9%;
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Σ
                                                                                                                                                           Created)
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                                                                       (Pseudomonas testosteroni).
ia; beta subdivision; Comamc
 Hurtubise
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IRON-SULFUR (2FE-2S) (;
IRON-SULFUR (2FE-2S) (;
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Pred. No. 5.9
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Pfam; PF00848; Ring_hydroxyl_A;
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U47637; AAC44526.1; -- HSSP; P23094; 1NDO. InterPro; IPR001281; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biphenyl/chlorobiphenyl dioxygenase genes: evolutionary among Gram-negative bacterial biphenyl dioxygenases."; Gene 174:195-202(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dioxygenase;
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (So or send an email to license@isb-sib.ch).
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-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron a
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            FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGETSYR
                                                                NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAG
                                                                                                                                                                                                     WGPLQARVETYKGLVFANWDPEAPDLKTYLSDAMPYMDVMLDRTEAGTEAIGGIQKWVIP
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                                                                                                                                                                                                                                                                                                              --TVFPTCSFLPGINTIRTWHPRGPNEVEVWAFVLVDADAPEDIKEEFRLQNIRTFNAGG
                                                                                           NQFRSAWGGHGAGWFINDSSILLSVVGPKITQYWTQGPAAEKAARRVPQLPILDMFGQHM
                                                                                                                     SGMGVLWDGY-----SGVHSADLVPELMAF--GGAKQERLNKEIGDVR-ARIYRSHL
                                                                                                                                                                                                                             ----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIK 192
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144; Conser
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Pred. No. 6.4e
73; Mismatches
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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BPHA_PSEPS
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SEQUENCE
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00348; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNG_HYDROXYL_ALPHA; 1.
PROSTITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons Catabolism; Oxidore
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M83673; AAA25743.1; -. HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taira K., Hirose J., Hayashida S., Furukawa K.;
"Analysis of bph operon from the polychlorinated biphenyl-d
strain of Pseudomonas pseudoalcaligenes KF707.";
J. Biol. Chem. 267:4844-4853(1992).

-i- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-
phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
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BPHA OR BPHA1.
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Q52028;
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                                                                                                                                                                                                                                                                Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Bacteria; Proteobacteria; gam
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15-JUL-1998 (Rel. 36, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
15-JUN-2002 (Rel. 41, Last annotation
15-JUN-2002 (Rel. 41, Last annotation
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                 11 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Heterohexamer consisting of three BphA subunits and each beta subunits. A ferredoxin (BphF) and a ferredoxin reductase (BphG) must be present to obtain activity (By similarity). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
COFACTOR: Binds 1 2Fe-2S cluster and 1 iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Biphenyl-polychlorinated biphenyl degradation pathway
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Pred. No. 6.
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IRON-SULFUR (2FE-2S)
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MEDLINE-88032840; PubMed=3667527;
ITIE S., Doi S., Yorifuji T., Takagi M., Yano K.;
"Nucleotide sequencing and characterization of the genes encoding benzene oxidation enzymes of Pseudomonas putida.";
J. Bacteriol. 169:5174-5179(1987).
-i. CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-idhydrobenzene-1,2-diol + NAD(+).
-i. COPACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-i. PACHMAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.
-i. SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS:
TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BUZA AND BNZB), A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988
01-NOV-1988
15-JUL-1999
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the Euro
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P08084;
EMBL; M17904; AAA25735.1; PIR; A29830; A29830.
                                                                                                                                                                                                      This
                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BNZA
                                                                  or send an email to license@isb-sib.ch).
                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE BACTER: DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                        FERREDOXIN (BNZC)
SIMILARITY: BELON
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                                                                                    license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
se alpha subunit (EC 1.14.12.3) (Pl subunit).
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952438;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12.18)
dioxygenase).
                                                                                                                                                                                                                             BPHA1
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Fukuda M., Yasukouchi Y., Kikuchi Y., Nagata Y., Kimbara K., Horiuchi H., Takagi M., Yano K.; "Identification of the bphA and bphB genes of Pseudomonas sp. : KKS102 involved in degradation of biphenyl and polychlorinated
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Pfam; PF00848; Ring_hydroxyl_A;
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                       SEQUENCE FROM N.A. MEDLINE=94324977; Pubmed=8048958;
                                                                                                                                                                                    Bacteria; Proteobacteria
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Aromatic hydrocarbons catabolism; Oxidoreductase;
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InterPro; IPR001663; Ring_hydroxyl_A.
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Local Similarity 32.5
- 142; Conservative
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32.98;
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Pred. No. 7.6e-39;
8; Mismatches 176;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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METAL
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Aromatic hydrocarbons catabolism; Oxide
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InterPro; IPR001663; Ring_hydroxyl_A.
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SUBUNIT: Heterohexamer consisting of 3 BphA1 subunits and 3 BphA2 subunits. A ferredoxin (BphA3) and a ferredoxin reduci (BphA4) must be present to obtain activity (By similarity).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
PATHWAY: Biphenyl-polychlorinated biphenyl degradation
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                                                                                                                                                                                                                                         ANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEGAGLQMT----SKYG
                                                                                                                                                                                                                                                                                                                                                 QCRHRGMRICRSDAGNAKAFTCTYHGWAYDIAGNLVNVPYEKEAFCDKKEGDC-GFDKAD
                                                                                                                                                                                                                                                                                                                                                                   VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEV-
                                                                                                                                                                                                                                                                                                                                                                                                                              PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGET
                                                                                                                                                                                                                                                                                                                                                                                                  SYRGFYRAYQAHVSSSNW
                                                                                                                             NCTVFPNNSMLTCSGVFKVWNPIDANTTEV----WTYAIVEKDMPEDLKRRLADSVQRTAG
                                                                                                                                                            SQFRAAWGGHGSGWFINDAAILMAVMGPKITQYWTQGPAAEKAAKRLNQMPTQTMFGQHM
                                                                                                                                                                                        SGMGVLWDGYSGVHSADLVPELMAFGGAK-----
                                                                                                                                                                                                                         CNWKFAAEQFCSDMYHAGTMAHLSGVLS---
                                                                                                                                                                                                                                                                                      WGPLQARVETYKGLIFANWDAEAPDLKTYLSDAMPYMDVMLDRTEAGTTVVGGMQKWVIP
                                AGGTFEQDDGENWVEIQRGLRGHKAKSAPLCAQMGLNVPNKSNPDFP----GKTAYVYAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
147; Conserv
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                                                                                             TVFPTCSFLPGINTIRSWHPRGPNEVECGPSWSSMPMR---PEDIKEEFRRQNIRTFN
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IRON (BY SIMILARITY).
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase;
                                                                                                                                                                            -QERLNKEIGDVRAR-IYRSHL
                                                                                                                                                                                                                       -SLPPE---MDLTQVQMSKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 458;
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Best Local :
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-92155191; PubMed-1740120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harayama S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
94
                        83
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                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: DEGRADATION OF BENZOATE AND TOLUATE TO CATECHOL. SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEINS: TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (XYLX AND XYLY), AN ELECTRON TRANSFER COMPONENT (XYLZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
HRGATLCRFRSGNKATHTCSFHGWTFSNSGKLLKVKDPKGAGYPDSFD--CDGSHDLKKV
                      HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKKCLG---LKEV
                                                DPRLFDLEMKHIFEGNWIYLAHESQIPEKNDYYTTQMGRQPIFITRNKDGELNAFVNACS
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                                                                                                                                                       454 AA;
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(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)
-dioxygenase alpha subunit (EC 1.14.12.-).
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                                                                                                   Conservative
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                                                                                                                                                                                                                                                NAD; Plasmid.
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226
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J. No. 7.7e-25;
---ches 135;
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            EMBL; AF009224; AAC46436.2; -.
PIR; S23477; S23477.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Elby D.M., Neidle E.L.;
Submitted (DEC-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for benzoate 1,2-dioxygenase reveal evolutionary multicomponent oxygenases."; 3. Bacteriol. 173:5385-5395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BD413 / ADP1;
MEDLINE-91358314; PubMed-1885518;
Neidle E.L., Hartnett C., Ornston
                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
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 Aromatic hydrocarbons
                                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO 84; 103-104; 171-172 AND 380-382
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                                                                                                                                                                                                                                                                                          COPACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. PATHWAY: DECRADATION PATHWAY: LEADING FROM BENZOATE TO CATECHOL SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEINS: TIMO SUBUNITS OF THE HYDROXYLASE COMPONENT (BENA AND BENB), AND AN ELECTRON TRANSFER COMPONENT (BENC).
                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: DEGRADATION
                                                                                                                                                                                                                                                                            DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                    NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQFGSQLRITRPLSVDRTEITIYCIAPKGETPRRARR 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMGVLWDGYSGVHSADLVPELMAFGGAKOERLNKEIGDVRAR-IYRSHLNCTVFPNNSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVEN-GADGYHVSTVHWNYAATQQQRKLRDAGDDIRAMTA--SSWGGDGGGFY---SFEN
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                                                                                                                                                      an
                                                                                                                                                                   requires a
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002 (Rel. 41, Last annotation update)
1,2-dioxygenase alpha subunit (EC 1.14.12.10).
                                                                                                                                                     email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel.
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                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
 catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                   Benzoate + NADH + O(2) =
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F BENZOATE TO 2-HYDRO-1,2-DIHYDROXYBENZOATE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P76253;
15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, I
16-OCT-2001 (Rel. 40, I
                                                                                  SEQUENCE FINAL MG1655;
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode M.A., Rose D.J., Pavis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli, and Escherichia coli 0157:H7.
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16-OCT-2001 (Rel. 40, Last annotation update)
Putative dioxygenase alpha subunit yeaW (EC 1
YEAW OR B1802 OR Z2845 OR ECS2511.
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                                                              complete genome sequence of nce 277:1453-1474(1997).
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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Pred. No. 7.
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RON (BY SIMILARITY).
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                                                                                                                                                           N.T., Burland V
K., Mayhew G.F.,
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                                                                                                                                                                                    Hypothetical NAD; Complete METAL
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DNA Res. 8:11-22(2001).

-I- COPACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

-I- SUBUNIT: PROBABLE HETERODINER OF YEAW AND YEAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Itch T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T. Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
                                                                                                                                          METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kirkpatrick Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                          EMBL; D90823; BAA15597.1; ALT_INIT. EMBL; D90824; BAA15606.1; ALT_INIT. EMBL; AE005403; AAG56791.1; -. EMBL; AP002558; BAB35934.1; -.
                                                                                                                                                                                                                  PROSITE; PS00570; RING_HYDROXYL_ALPHA;
Hypothetical protein; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000274; AAC74872.1;
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MEDLINE=21156231; PubMed=11258796;
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MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                          InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                               EcoGene; EG13509;
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                                            10.2%; 26.6%;
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Pred. No. 5.1e
53; Mismatches
                                                                                                         IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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No. 5.1e-12;
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15-JUN-2002
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      betaine synthesis.

CATALYTIC ACTIVITY: Choline + 2 reduced ferredoxin + O(2) betaine aldehyde + 2 oxidized ferredoxin + H(2)O.

COTACOR: Magnesium. Probably binds a 2Fe-2S group and an atom (By similarity).

PATHWAY: Osmoregulatory choline-glycine betaine pathway.

SUBCELULIAR LOCATION: Chloroplast stroma (By similarity).

SUBCELULIAR LOCATION: Chloroplast stress.

INDUCTION: By salt, drought and heat stress.
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"Isolation of a Choline monooxygenase cDNA clone from Amaranthus tricolor and its expressions under stress conditions.";
Cell Res. 11:187-193(2001).
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                                                      Pfam; PF00355; Rieske; 1.
Monooxygenase; Oxidoreductase; Chloroplast; Iron-sulfur;
                                                                                                                                                       EMBL; AF290974; AAK82768.1; -.
                                                                                                                          InterPro;
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(Rel. 41, Last sequence update)
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Search completed: January 27, Job time: 8.33333 secs
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                                            IN-RSEFPMESNWKVFCDNYLDSAYHVPYAH 295
                                                                 VGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                                                            KKCLGLKEVARVESFHGFIYGCFDQEAPP-----LMDYLGDAAWYLEPMFKHS--GGLEL
                                                                                                                                  GQGKVHAFHNVCTHRA-SILACGTGKKSCFVCPYHGWVFGLDGSLMKATKTEN---QVFD
                                                                                                                                              NDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLN 129
                                                                                                                                                                             AEDGFTPPSTWYTDPSLYSHELDRIFSKGWQVAGYSDQIKEPNQYFTGSLGNVEYLVCRD 153
                                                                                                                                                                                                  SESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQ
                                                                                      PKELGLVTL-KVAIWGPFVLISLDRSGSEGTEDVGKEWIGSCA---EEVKKHAFDPSLQF
                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                    442
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167
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187
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                                                                                                                                                                                                                                                                    MW;
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IRON-SULFUR (2FE-2S) (E
IRON-SULFUR (2FE-2S) (E
IRON-SULFUR (2FE-2S) (E
IRON-SULFUR (2FE-2S) (E
                                                                                                                                                                                                                                   Score 239.5;
Pred. No. 2.
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IRON (POTENTIAL).
; C7520F16EAA67A0E CRC64;
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Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                   69
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7;



GenCore version 5.1.3 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 08:55:37 ; Search time 13.1667 Seconds (without alignments) 3278.305 Million cell updates/sec

Title: Perfect score: US-09-843-250-33 2408

Sequence: 1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	0	5	4	ω	2	_	No.	Result
312.5	330	336.5	387.5	393	407.5	410.5	417	450	585	588.5	603	615	615	615.5	637	648.5	650.5		735	735	735	772	955	2051	2290	2344	2402	2402	Score	
13.0	13.7	14.0	16.	16.	16.	17.	17.		24.3			•	•	•	•	•	•			٠	٠	•	•		•		•	8	Match L	% Query
391	426	424	464	461	455	454	471	469	458	448	431	458	457	459	461	450	450	455	453	453	453	450	459	447	449	449	462		ength	
2	N	N	N	N	2	N	N	ν	N	٢	N	Ľ	1	1	Ν	1	1	N	2	Ν	N	N	N	2	2	N	N	2	BB	
T31251	T31278	E83384	G83331	S23477	E83332	A41659	T31281	T50934	JC2467	A29830	3W0098	A42409	JC4993	в41858	S51757	A36516	JN0812	T31258	G85898	D91054	A65031	T31256	T31134	JC5352	C55217	JN0644	S27632	JS0071	ID	
O		probable ring-hydr	\vdash	probable benzoate	\mathbf{r}		benzoate 1,2-dioxy	dioxygenase DitA1,	biphenyl dioxygena	benzene 1,2-dioxyg	carbazole dioxygen	_				toluene dioxygenas	_	O	biphenyl dioxygena	biphenyl dioxygena		terminal oxygenase	naphthalene dioxyg	2-nitrotoluene dio	polycyclic aromati	Ľ	lene	hthalene	On	

choline monooxygen	T08550	N)	426	7.7	186	45
2-nitrotoluene dio	2 JC5354	N)	186	8.9	214.5	44
choline monooxygen	T09214	N	439	9.3	223	43
choline monooxygen	T14542	ь. Б	44(9.3	224	42
probable dioxygena	2 G70946	N	383	9.7	233.5	41
probable choline m	В64941	-	374	10.2	246	40
probable choline m	2 G90942	- N	374	10.2	246	39
probable choline m	2 C85791	- N	37,	10.2	246	38
	2 AF0304	~	37	10.4	249.5	37
biphenyl dioxygena	T31285	N	420	10.9	263	36
Rieske 2Fe-2S fami	187635	~	40,	11.2	269.5	35
benzoate 1,2-dioxy	AG3320	о. N	41!	11.8	283	34
probable aromatic-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	N	417	11.9	287	ω ω
probable ring hydr	F82970	N	429	12.1	291	32
ring hydroxylating	2 AH2665	N	468	12.9	311.5	31
hypothetical prote	2 G97447	ω N	468	12.9	311.5	30
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ALIGNMENTS

γo	Qу	Фр	Qy Db	Qу	Qу	Qy Db	Que Bes Mai	A;Crc C;Cou C;Ge A;Ge C;Su C;Ke; F;71	R; Ku Gene A; Ti A; Re A; Ac A; Mo A; Res	RESULT JS0071 naphth C;Spec C;Date C;Acce
361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES 360 	241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 	181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 	121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 	61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 	1 MNYNNKILVSESGLSOKHLIHGDEELFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60 	Query Match 99.8%; Score 2402; DB 2; Length 449; Best Local Similarity 99.8%; Pred. No. 1.3e-183; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	A;Cross-reterences: GB:M23914; NID:q151392; PION:AABA7591.1; PID:q151394 C;Comment: Naphthalene dioxydenase system is composed of three proteins. C;Genetics: C;Genetics: C;Genetics: C;Guperfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: Toluene dioxygenase chain; Rieske [C;Superfamily: Toluene dioxygenase chain; Rieske	Teeri, T.H. genes en aracterization of genes en MID:3243438	RESULT 1 JS0071 naphthalene dioxygenase (EC 1.14.12) ndoB protein - Pseudomonas putida C;Species: Pseudomonas putida C;Species: Pseudomonas putida C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999 C;Accession: JS0071

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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 14-462 < DE2>
A; Cross-references: GB:M60405; NID:g151195; PIDN:AAA16125.1; PID:g294351
A; Cross-references: GB:M60405; NID:g151195; PIDN:AAA16125.1; PID:g294351
A; Experimental source: strain C18
C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; C; Superfamily: toluene dioxygenase terminal oxygenase; Rieske iron-sulfur protein; B4-13Z/Domain: Rieske [27e-25] homology <RSK>
F; 94,95,114,117/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
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A:Title: Metabolism of dibenzothiophene and naphthalene A:Reference number: A49343; MUID:94042852; PMID:8226631
A:Accession: B49343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfu (;Species; Pseudomonas sp. C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #te C;Accession: S27632; B49343 R;Denome, S.A.; Young, K.D. submitted to the EMBL Data Library, February 1992 A;Bescription: Cloning and molecular characterization A;Reference number: S27631 A;Accession: S27632
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A; Residues: 1-462 < DEN>
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                                                                            QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                                                                           FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
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Pred. No. 1.4e-183;
0; Mismatches 1;
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A;Title: Identification and A;Reference number: A55217; A;Accession: C55217 A;Status: preliminary
                                                                                         polycyclic aromatic hydrocarbon dioxygenase (EC 1.14.12.-) iron-sulfur C;Species: Pseudomonas putida C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 20-Jun-C;Accession: C55217
                                                            R;Takizawa, N.; Kaida, N.; Torigoe, J. Bacteriol. 176, 2444-2449, 1994
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Best Local :
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C;Superfamily: toluene dioxygenase terminal oxygenase component larse C;Keywords: 2Fe-2S; heterotetramer; metalloprotein; oxidoreductase; F;71-119/Domain: Rieske [ZFe-2S] homology cRSK> F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: JN0644
R;Simon, M.J.; Osslund, T.D.
Gene 127, 31-37, 1993
A;Title: Sequences of genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Pseudomonas putida
C;Date: 31-Dec-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfur oxygenase N;Alternate names: nahAc protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIFAPGDYVTAKMG
                     QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                  DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                   ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                  KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIFARNWLFLTHDSLIPSPGDYVTAKMG
QAHVSSSNWAEFEDASSTWHTELTKTTDR
                                                                               DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                            FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTEGPAGFWES
                                                                                                                                                                                                       FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
                                                                                                                                                                                                                                              QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGSKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                             ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFASLAGNAVLPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                               KELYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPIFKHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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96.7%;
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characterization MUID:94209249; PM

on of genes encoding PMID:8157615

polycyclic

aromatic

s:;

Moritani, T.;

Sawada,

T.;

Satoh, S.;

Kiyohara

20-Jun-2000

protein

large

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A;Gene: ntdAc C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R:C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R:C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;69-117/Domain: Rieske [2Fe-2S] homology <RSK> F;79,81,99,102/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #sf
                                                                                                                                                                                                                                                                                                                                      R.Parales, J.V.; Kumar, A.; Parales, R.E.; Gibson, D.T. Gene 181, 57-61, 1996
A.Title: Cloning and sequencing of the genes encoding 2-nitrotoluene dioxygenase A.Reference number: JC5350; MUID:97128768; PMID:8973308
A.Accession: JC5352
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A:Rosidues: 1-449 <TAK>
A:Residues: 1-449 <TAK>
A:Residues: 1-449 <TAK>
A:Residues: 1-450 <TAK
A:Residues:
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C;Date: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Aug-1999
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                Score 2051; I
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34; Mismatches
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Pred. No. 1.1e-174;
3; Mismatches 12;
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                DB 2;
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                     QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                           FPNNSFLTGSATEKVWNPIDENTTEVWTYAFVEKDMPEDLKRRLADAAQRSIGPAGFWES
                                                                                                                                                                                  FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
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QAHISSSNWAEFENASRNWHTELTKTTDR
                                                                              DDNENMETLSQNAKKYQSSNSDQTASLGFGKDVYGDECYPGVVGKSAIGETSYRGFYRAY
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A; Molecule type: DNA
A; Residues: 1-459 <ROI
A; Cross-references: EN
C; Genetics: A;Genome: plasmid pNL1 C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Ri C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;80,82,100,103/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #: R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; I submitted to the EMBL Data Library, July 1998 A;Description: Complete sequence of a 184 kb (naphthalene dioxygenase (EC 1.14.12.-) large chain - Sphingomonas aromaticivorans C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000 C;Accession: T31134 A; Gene: bphAlf A; Status: preliminary; A; Reference number: A; Accession: T31134 A; Description: Complete sequence A; Reference number: Z20992 Query Match al Similarity 43.9 192; Conservative <ROM> EMBL:AF079317; NID:g3378261; PID:g3378275; PIDN:AAD03858 translated 39.7**%**; 43.9**%**; Score 955; DB 2; Pred. No. 3.3e-68; 1; Mismatches 162 from GB/EMBL/DDBJ catabolic Thurston, Length 459 S.J.; plasmid Sisk, from E.C.; Sphingomonas Rieske #status 0 Ξ

GKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAA-LPPEGAGLQMTSK

LDKSKLGLAPI-RVETYKGFIFGCHDPEAPSLEDYLGDFCWYLDTIWDGPDGGLELLGPP LNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK-HSGGLELVGPP 186

185

LVDNANASQSRRVFWDQDVYQLELERIFSRCWLMLGHDSLVPKPGDFITTYMAEDRVILS LVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVS

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RQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGES

RQPDGSLKAFINSCTHRGNQICHADSGSAKAFVCNYHGWVFGQDGSLVDVPMEERCYHSD 126

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417

YRAYQAHVSSSNWAE 431

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A:Note: bphAla
C:Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
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A;Description: Complete sequence of a 184 kb catabolic A;Reference number: Z20992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal oxygenase component large chain homolog - C;Speciles: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 C;Accession: T31256 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurst
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A; Status: prelimina
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LFDNDDGDNLTACTEQSRGWRTAQMDVYTNMALGRSGKREG-FPGDIAAGLVSEHNQRYF
                                FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGF
                                                                                                          NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAG
                                                                                                                                              -GLSVAGMNGHMVLSALDGVSGYAFYPDPKPILEYLEANRQTVIDRLGEVRGRQVWGAQV
                                                                                                                                                                               AGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHL
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-19, 'A', 21-383, 'ATAPATANCVWKW', 397-398, 451, 'R', 453, 'SAATTAFLALLTISFQKLPL
A;Cross-references: EMBL:237966; NID:g550595; PIDN:CAA86018.1; PID:g550596
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;75-123/Domain: Rieske [2Fe-2S] homology <RSK>
F;85,87,105,108/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
C;Accession: A65031; S49292
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.A.; Rose, D.J.; Mau, B.;
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                                                                                              YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK
                                                                                                                                                                GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
                                                                                                                                                                                                                 AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
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                                                                                                                                     GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA
                                                                                                                                                                                                                                                      RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTA
                                                                                                                                                                                                                                                                                              QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----AEQRLGEVRALRL
                                                                                                                                                                                                                                                                                                                                   --PEGAGLOMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
                                                                                                                                                                                                                                                                                                                                                                              AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCRHRAMRVSYADCGNTRAFTCPYHGWSYGINGELIDVPLEPRAYPQGLCKSHWGLNEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYTDPDIYQLELERIFGRCWLFLAHESQIPKPGDFFNTYMGEDAVVVVRQKDGSIKAFLN
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Mau, B.; Shao, Y.
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Pred. No. 1.1e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                   -RSGESIFSSLAGNAALP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #text_change 01-Mar-2002
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blibhenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component C:Species: Escherichia coli C:Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: G85898 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                  RESULT
G85898
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C; Superfamily: toluene dio:
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:BA000007; PIDN:BAB36827.1; PID:g13362875; A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic E:
^-Deference number: A99629; MUID:21156231; PMID:11258796
A; Molecule 1
A; Residues:
                                                  A; Reference number: A85480; A; Accession: G85898
                                                                   A; Title: Genome sequence of enterohemorrhagic Escherichia coli A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                      iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biphenyl dioxygenase (EC 1.14.-.-) C; Species: Escherichia coli
                                   A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-453 <HAY>
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                                   preliminary
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                                                                                                                                                                                                                                                                                                                                           YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                                                                                                                                                                                                                                                              GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
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                                                                                                                                                                                                                                                                                                         ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
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 type: I : 1-453
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Yasunaga, T.; Kuhara, S.;
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Pred. No. 1.1e-
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Shiba, T.;
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                                                                                                                     J.D.; Rose, Potamousis,
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aromatic oxygenase large chain - Sphing
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 *sequence_revision
C;Accession: T31258
R;Romine, M.F.; Stillwell, L.C.; Wong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005174; NID:g12516944; PIDN:AAG57651.1; GSPDB:GN00145; UWGP:A;Experimental source: strain O157:H7, substrain EDL933 c;Genetics: A;Gene: hcaAl c;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske C;Keywords: oxidoreductase
                                                           R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic
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A; Status: preliminary; translated
                     A; Reference number: A; Accession: T31258
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                                                                                                                                                                                                                                                                                            ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
                                                                                                                                                                                                                                                                                                                                YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK
                                                                                                                                                                                                                                                                                                                                                                                                               GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                                                                                                                                                                         GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----AEQRLGEVRALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYTDPDIYQLELERIFGRCWLFLAHESQIPKPGDFFNTYMGEDAVVVVRQKDGSIKAFLN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
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65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%;
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                                                                                                                                                                                   Sphingomonas aromaticivorans plasmid pNL1
    from
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Pred. No. 1.1e-50;
4; Mismatches 174
    GB/EMBL/DDBJ
                                                                                                                                               11-Jan-2000
                                                                                                                                                                                                                                                                                                                                445
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                                                                                                    S.J.; Sisk, E.C.; Sensen,
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                                                                                                    C.W.
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A; Genome: plasmid pNL1
A; Note: bphAib
C; Superfamily: toluene
C; Keywords: 2Fe-2S; met
F; 88, 90, 108, 111/Binding
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C;Genetics:
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A; Residues: 1-455 < ROM>
                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: toluene dioxygenase terminal oxygenase component large chain; Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein; Riesk
                                                                                                                                                                                                                             Matches
                                                                                                                                                                              Local 153;
     11
NYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGI
                                                                                                                                                                                                                       Similarity 36...
53; Conservative
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                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                       Score 723.5; DB 2
Pred. No. 9.2e-50;
3; Mismatches 169
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A;Experimental source: strain ML2
C:Comment: This enzyme is involved in catalyzing the oxidation of benzene to cis-1,2-dil C:Comment: The reduced enzyme catalyzes the oxidation of benzene to cis-benzene dihydroc
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Best Local S
Matches 148
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   195
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                                                                                                                                                                                                                                                                                     Local Similarity
                               PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
                                                                                                                                                                                                               YQRW
WKAPAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
                                                                        --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
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                                                                                                                 QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA--
                                                                                                                                                  VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE--
                                                                                                                                                                                         IYTDEDLYQLELERVFARSWLLLGHETHIRKPGDYFTTYMGEDPVVVVRQKDASIAVFLN
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9; Mismatches
                                                                                                                                                                                                                                                                                                       Score 650.5;
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6e-44;
                                                                                                                                                                                                                                                                   174;
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EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP
                         TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS
                                                                        PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
                                                                                                                                                    GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
                                                                                                                                                                                       VLWDGYSGVHSADLVPELMAF - -GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                              WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL-----EMADLAPPTVGKQYRASWGGHGS
                                                                                                                                                                                                                                                    WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                                                       PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                                                                                                                                                                                                                                                                        --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                                                                                                                                                                                                                                 QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA----
                                                                                                                                                                                                                                                                                                                                                                                                                  VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLN
                                                                                                           TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWESDDNDNME
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CLNKKEWS

94

263

321 307

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367

208

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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-450 <ZYL>
A; Cross-references: GB:J04996; NID:g151600;
A; Cross-references: Strain F1
                                                                                                                                     C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidorec F;86-134/Domain; Rieske [2Fe-2S] homology <RSK> F:96-98,116,119/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               toluene dioxygenase (EC 1.14.12.11) terminal oxygenase component large c;Species: Pseudomonas putida C;Date: 15-Feb-1991 #sequence_revision 06-Jan-1995 #text_change 18-Jun-C;Accession: A36516
                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 264, 14940-14946, 1989
A;Title: Toluene degradation by Pseudomonas
A;Reference number: A36516; MUID:89359301; F
A;Accession: A36516
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                                                                           Local Similarity
KMMTSPDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP---
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                                                         Conservative
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                                                71;
                                                                           Score 648.5; DB 1
Pred. No. 8.7e-44;
                                                         Mismatches
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PMID:2670929
                                                                                                                                                                                                                                                                                          PIDN: AAA26005.1;
                                                                                                 DB 1;
                                                         181;
                                                                                               Length 450;
                                                         Indels
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submitted to the EMBL Data Library, July 1994
A;Description: Evolutionary relationship of the
A;Reference number: S51757
A;Accession: S51757
A;Molecule +---
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A;Experimental source: strain P6
C;Genetics:
A;Gene: bphA1
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;89-137/Domain: Rieske [2Fe-2S] homology <RSK>
F;99,101,119,122/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #statu
                     RESULT 15
B4185B
B4185B
biphenyl dioxygenase (EC 1.14.12.-) terminal oxygenase component
C:Species: Pseudomonas sp.
C:Date: 04-Mar-1993 #sequence_revision 06-Jan-1995 #text_change 0
C:Accession: B4185B
R:Erickson, B.D.; Mondello, F.J.
J. Bacteriol 174, 2903-2912, 1992
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S51757
biphenyl dioxygenase (EC 1.14.-.-) large chain - Rhodoccoccus globerulus
C;Species: Rhodoccoccus globerulus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S51757
C;Accession: S51757
R;Asturias, J.A.; Diaz, E.; Timmis, K.N.
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A; Residues: 1-461 <AST>
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Nucleotide sequencing and transcriptional mapping of the genes encoding bipheny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGMGVLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVRARIYRSHLNCTVFPNNS
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                                                                                 #text_change 05-May-2000
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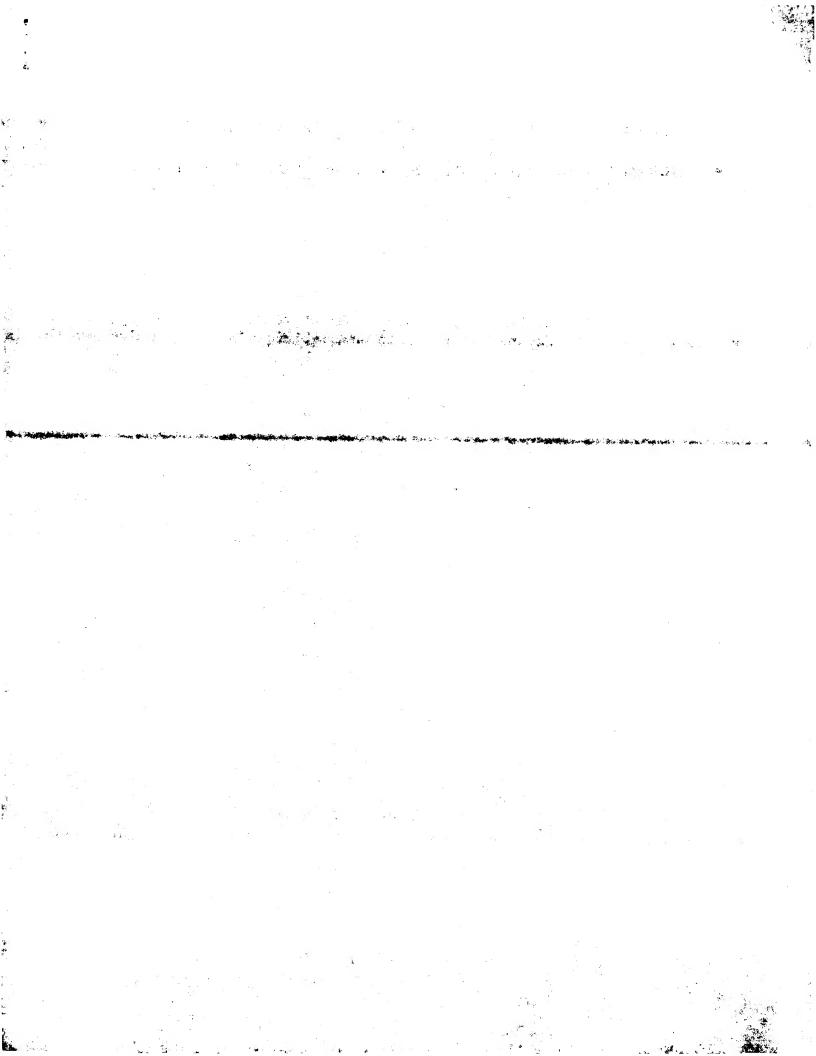
Search completed: January 27, 2003, 09:03:46

Job time : 14.1667 secs

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C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; F;90-138/Domain: Rieske [2Fe-2S] homology <RSK> F;100,102,120,123/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #stat
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A;Accession: B41858
A;Molecule type: DNA
A;Residues: 1-459 <ERI>
A;Cross-references: GB:886348; NID:9349602; PIDN:AAB63425.1; PID:9151084
A;Experimental source: strain LB400
A;Rote: sequence extracted from NCBI backbone (NCBIN:97256, NCBIP:97259)
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Best Local Similarity
432
                                       407
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                                                                                                         SVQRTAGFAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                  KCLGLKEV-----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN
VYAEEAARGMYHHWMRMMSEPSWA
                                     AIGETSYRGFYRAYQAHVSSSNWA 430
                                                                                                                                                          VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR
                                                                                                                                                                                                                                    QIPTK-GNQFRAAWGGHGSGWYVDEPGSLLAVMGPKVTQYWTEGPAAELAEQRLGHTGMP
                                                                                                                                                                                                                                                                                                                 GGMQKWVIPCNWKFAAEQFCSDMYHAGTTTHLSGILAG----
                                                                                                                                                                                                                                                                                                                                                      GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKGLLDPR-IYADQSLYELELERVFGRSWLLLGHESHVPETGDFLATYMGEDPVVMVRQK
                                                                            HNIRNESAGGVEEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y
                                                                                                                                                                                             VRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
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Pred. No. 3.8e-41;
455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
        Match
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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AAB12581
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Oxidase amino acid	AAW80332	19	405	5.2	126
Rieske motif in D	AAW79020	19	35	•	164
Rieske motif in G	AAW79019	19	35	٠	173
Rieske moti	AAW79018	19	35	7.5	181
Novel human dia	ABG18089	22	9		182
Herbicidally	ABB93163	23	426	•	186
Human oxygenase	ABP35375	23	99	•	196
Spinach ch	AAW69562	19	439	٠	223
Sugarbeet cholin	AAW69563	19	446	9.3	224
Atriplex hortens	ABB06798	23	438	9.7	233
C album choline		22	433		235
C album choline	AAG62633	22	433	•	235
C album choline m	AAG62634	22	ω		239
Pseudomonas aerug	AAU33601	22	N		336.5
೦೦	AAB79227	22	9		356
	AAG92386	22	9	5	375
Klebsiella pneumo	AAU36099	22	385	5	7
	AAR32085	14	N	2	552.5
Chimeric PCB	AAY81989	21	ū	5	613
Chimeric	AAY81990	21	ū	5	616
Aromatic dil	AAR66729	16	S	5	N
Terrabac	AAO17350	23	4	7.	658.5
Benzene ring	AAY83939	21	ø	7.	ŧл
E. coli cellular	AAU34660	22	ū	30.5	735
Burkholderia	AAB29474	21	452	5	1093
NDO related	AAB12576	21	451	Η.	1968.5
NDO related	AAB12575	21	447	85.2	2052
NDO related comp	AAB12574	21	447	0	2189
NDO related	AAB12573	21	449	2.	2219
NDO related comp	AAB12572	21	449	5	2292
NDO related	AAB1257]	21	449	ა	2318
NDO related	AAB1257(21	449	7.	2346
NDO related compl	AAB12569	21	449	9	2394
Naphthalene dioxy	AAB12584	21	448	9.	2397
NDO related comple	AAB12568	21	449	.6 9.6	2399

ALIGNMENTS

AAB12579 standard; Protein; 449 AA

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WPI; 2000-452174/39.
N-PSDB; AAA65353.
                                                                                                                                                                                                  Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral diol; polymer; resin; pharmaceutical; rubber industry; bioremediation.
Novel naphthalene dioxygenase mutant having a specific amino acid
                                                                                                            26-OCT-1999;
                                                                                                                                                    WO200037480-A1
                                                                                                                                                                       Synthetic.
                                                                                                                                                                                Pseudomonas sp
                                                                                                                                                                                                                                      Naphthalene dioxygenase mutant F352A protein sequence
                                                                                                                                                                                                                                                              09-NOV-2000
                                                                    (IOWA ) UNIV IOWA RES FOUND
                                                                                         26-OCT-1998;
                                                                                                                                29-JUN-2000
                                                  Gibson
                                                                                                                                                                                                                                                            (first entry)
                                                                                         98US-0105575
                                                                                                            99WO-US25079
                                                  Ď
                                                   Resnick
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                                                  Lee
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Naphthalene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
AAB12565
                                 AAB12565 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dihydrodiol, (18,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \mathbf{L}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG 60
                                                                                                                     DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                   FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
                                                                                                                                                                                                                                                                                                                                                         QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                  ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                             DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                       QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                             ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (I)
                               Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on describes a naphthalene dioxygenase comprising several polypeptides which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No. 1.4e-225;
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The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (I) comprising several polypeptides which contain an alpha submit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1S,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,
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                                                                                                                                                                                                                                                                             Claim
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                                                                                                         WO200037480-A1
                                                                                                                                                             Synthetic
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26-OCT-1999;

99WO-US25079

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CC related complex (I) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)(1S,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydronaphthalene respectively. The polypeptides and CC the host cells are also useful for preparing 1,2-dihydroxy-1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which CC involves contacting them with phenanthrene. The polypeptides and CC the host cells are also useful for preparing 1,2-dihydroxy-1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which CC involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, cells are also used in bioremediation in which they oxidise an CC accorresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer. CC cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer. CC anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC exemplification of the present invention.
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N-PSDB; AAA65341.
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nes 448; Conserv
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KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                       FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES
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                                    C(-)-(15.2R)-cis-naphthalene dihydrodiol, (- or +)-cis-bibhenyl-3,4-cidihydrodiol, (15.2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cidihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, cidihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
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  449
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                                                                                        Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
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bioremediation
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Claim

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Page 129-131;

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Best Local :
                                                                       09-NOV-2000
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Pseudomonas sp.
                                  Naphthalene
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                                 dioxygenase mutant F352L protein sequence
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strain NCIB 9816-4; naphthalene dioxygenase;
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Pred. No. 3
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(-)-(15.2R)-(15.napththalene dihydrodiol, (-or +)-(15.bhphenyl-3.4-(25.cd dihydrodiol, (15.2R)-cis-haphthalene, 1.2-dihydrodiol, cis-1,2-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.4-(25.bhphenyl-3.bhphenyl-3.4-(25.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bhphenyl-3.bh
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polymer; resin; pharmaceutical; rubber industry; bioremediation.
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dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene
                                                                                                                                                                           The present invention describes a naphthalene dioxygenase (NDO) or NE related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                      Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDC inducible multi-component enzyme; alpha subunit; mutant; chiral polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                           Claim
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Best Local
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                                                                                                                                                              Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d polymer; resin; pharmaceutical; rubber industry; bioremediation.
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                               (IOWA ) UNIV IOWA RES
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Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation pharmaceutical or rubber industry and for carrying out bioremediation pharmaceutical or rubber industry and for carrying out bioremediation pharmaceutical or rubber industry and for carrying out bioremediation pharmaceutical or rubber industry and for carrying out bioremediation involves complex (1) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, and 1,2-dihydronaphthalene, and 1,2-dihydronaphthalene, and 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-
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                                                            DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cemplification of the present invention.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(18.2R)-cis-raphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (18,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,2
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99.8%;
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The present invention describes a naphthalene dioxygenase (NDO) or Net lated complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1.5,2R)-cis-naphthalene dihydrodiol, (-0-+)-cis-biphenyi-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1.2-dihydrodiol, cis-1.2-dihydrodiol, (15,2R)-cis-phenanthrene-1.2-dihydrodiol, cis-1.2-dihydrodiol, (15,2R)-cis-phenanthrene-1.2-dihydrodiol, cis-1.2-dihydrodiol, (15,2R)-cis-phenanthrene-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol, cis-1.2-dihydrodiol

Claim 13;

Page 102-103; 151pp;

English

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RESULT 12
AAB12584
ID AAB12
XX Induc
XX Induc
KW Pseud
KW Pseud
KW Polyn
XX Induc
XX Synth
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                                                                                                       Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral c
                                                                                                                                                                                                                                                                    AAB12584 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxphenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
                                                                                                                                                         Naphthalene dioxygenase mutant F352Y protein sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                       QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                          QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                             DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                           DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFCSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
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                                                                                      pharmaceutical;
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99.6%;
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Pred. No. 1.1e-224;
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                                                                                      industry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
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KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180

KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL

180

IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG

IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE

FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES

FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTYGPAGFWES

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involves contacting them with naphthalene, biphenyl, phenanthrene, clindene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which clinvolves contacting them with phenanthrene. The polypeptides and the close cells are also used in bioremediation in which they oxidise an index cells are also used in bioremediation in which they oxidise an cc aromatic compound such as indene, 1,2-dihydronaphthalene, cells are useful for preparing fluorene, dibenzofuran, cc dibenzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, cc dibenzochiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cc cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cc exemplification of the present invention.
                                                                                    Query Match
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                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related complex (I) comprising several polypeptides which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 144-145; 151pp; English
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DB; AAA65377.
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Score 2397; DB 21;
Pred. No. 1.6e-224;
0; Mismatches 1;
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RESULT 13
AAB12569
ID AAB12
cc dihýdroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which crimvolves contacting them with naphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydronaphthalene respectively. The polypeptides and cc indene, and 1,2-dihydronaphthalene respectively. The polypeptides and cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-c dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which convolves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an convolve compound such as indene, 1,2-dihydronaphthalene, oxidise an convolve cells are anotheracene, phenanthrene, dibenzo(1,4)dioxan, compound, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 104-105; 151pp; English.
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N-PSDB; AAA65343.
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09-NOV-2000
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                                       AAB12571;
                                                                             AAB12571 standard; Protein; 449 AA
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                                                                                                                                                                              QAHVSSSNWAEFEDASSTWHTELTKTTDR 449
                                                                                                                                                                                                     QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                                 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
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                                                                                                                                                                                                                                                              DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                    DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                            FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                          QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGSKQERLNKEIGDVRARIYRSHLNCTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPIFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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(first entry)
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96.78;
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Pred. No. 1.5e-219;
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dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which convolves contacting them with naphthalene, biphenyl, phenanthrene, involves contacting them with naphthalene, biphenyl, phenanthrene, convolves contacting them with phenanthrene. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-convolves contacting them with phenanthrene. The polypeptides and the involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, dibenzo(1,4)dioxan, conveyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, cacenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cxemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                               61
MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG
                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
429; Conser
                                                                                                                                                                                              MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIXARNWLFLTHDSLIPSPGDYVTAKMG
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%;
95.5%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                2318; DB 21;
No. 8.2e-217;
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В

	_	421	Db
	QAHVSSSNWAEFEHASSTWHTELTKTTDR 449	421	Qy
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360	FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES	301	Оу
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300	QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV	241	Qy
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180	KELYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPSLMDYLGDAAWYLEPIFKHSGGL	121	Db
180	- L	121	QY

Search completed: January 27, 2003, 08:58:48 Job time: 30.1667 secs

OM protein - protein search, using sw model Run on: January 27, 2003, 09:02:32; Search time 7 Seconds (without alignments) 1294.310 Million cell updates/sec GenCore version 5.1.3 Compugen Ltd.

Title: Perfect score: 2409 US-09-843-250-34

Scoring table: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 1 MNYNNKILVSESGLSQKHLI......AEFEHASSTWHTELTKTTDR 449

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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735 375.5 336.5 336.5 185 1174 174 110 110 110 110 110 110 110 110 110 11	Score
130 145 155 165 175 175 175 175 175 175 175 175 175 17	Query Match Length
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Query Match Best Local Similarity

30.5%;

Score 735; DB 10; Pred. No. 1.8e-57;

Length 453;

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	Sequence 16, Appl	Sequence 16, Appl	Sequence 1362, Ap	Sequence 46, Appl	Sequence 46, Appl	Sequence 246, App	Sequence 17, Appl	Sequence 17, Appl	Sequence 45, Appl	Sequence 44, Appl	Sequence 45, Appl	Sequence 44, Appl	Sequence 6115, Ap	Sequence 10, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 15, Appl	Sequence 9, Appli	Sequence 9, Appli	addresses to abba

ALIGNMENTS

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				2001-0	FILING DATE:		٠.
			/269,308	z			٠.
			2	2000-13	FILING DATE:		٠.
			/257,931	z		PRIOR AP	٠.
			7	2000-11	FILING DATE:	PRIOR FI	٠.
			60/253,625	NUMBER:	APPLICATION	PRIOR AP	٠.
			ω	2000-10	FILING DATE:	PRIOR FI	٠.
			60/242,578	NUMBER: 60,	APPLICATION	PRIOR AP	٠.
			5	2000-05-26	FILING DATE:		٠.
			60/207,727	NUMBER: 60,	APPLICATION	PRIOR AP	٠.
			ω	2000-05-23	FILING DATE:	PRIOR FI	٠.
			60/206,848	NUMBER: 60,	APPLICATION	PRIOR AP	٠.
			_		FILING DATE:	PRIOR FI	٠.
			60/191,078		APPLICATION NUMBER:	PRIOR AP	٠.
			3-21	0	FILING DAT		٠.
		242	US/09/815,242		APPLICATION NUMBER:	CURRENT	٠.
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				Howard	••	APPLICANT	٠.
			Ŧ.	Yamamoto, Robert	••	APPLICANT	٠.
				Carr, Grant J.	••	APPLICANT	٠.
				Trawick, John D.		APPLICANT	٠.
				Wall, Daniel	••	APPLICANT	٠.
			Σ.	ith	••	APPLICANT	٠.
				, Kari L.	T: Ohlsen,	APPLICANT	٠.
				ck, Robert	WT: Haselbeck,	APPLICANT:	٠.
					GENERAL INFORMATION:	GENERAL I	٠.
				61569A1). US20020C	Patent No	٠.
			US/09815242		ce 10253, Application	Sequence	٠.
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Sequence 11692, Application US/09815242 Patent No. US20020061569A1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert
                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                      APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                        APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD------GQTARPVWETAKDALQFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYTDPDIYQLELERIFGRCWLFLAHESQIPKPGDFFNTYMGEDAVVVVRQKDGSIKAFLN 83
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
Trawick, John D.
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  pneumoniae
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                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                              SEQ ID NO 6140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                        Query Match
Best Local
                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 LNADVQPLEAYLGETCKIIDLIVDQAPEGLEVLKGSSSYVYEGNWKLGAEN-GADGYHVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 FDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAENFVGDAYHVG 210
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80
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                                                                                                                                                        Local Similarity
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                                                                                     IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
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YOKOI, HARUHIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENOH, AKIHIRO
                                                                                                                                   Conservative
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                                                                                                                                 15.6%; Score 375; DB 9; 26.3%; Pred. No. 1.8e-25; tive 66; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
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Pred. No. 1.
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1.2e-25;
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                                                                                                                                                                             Length 490;
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                                                                                                                                 Gaps
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US-09-815-242-11692

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Carr, Grant

APPLICANT: APPLICANT:

Xu, H. Howard

FILE REFERENCE: ELITRA.011A

NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for SEQ ID NO 11692 LENGTH: 385

ORGANISM: Klebsiella

TYPE:

PRIOR FILING DATE:

PRIOR PRIOR PRIOR PRIOR PRIOR

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204

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                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5097
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; Sequence 5097, Application

; Patent No. US20020061569A1
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                                         Matches 114;
                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                          PRIOR APPLICATION N
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 GVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPNNSML-T 308
25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
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                                         Conservative
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                                     Score 336.5; D
Pred. No. 3.9e-
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US-09-776-490-19
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                                                                                               INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 28234
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray, John TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EILESCQ---RAYAH-----AALGYSDFSRG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWESDDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VYRNFLFIHYGARQASLETYLGQAKDYIDLICDQSEAELEIIPGGFEHSIKANWKLLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDILGLN--IRSFFPTAADEVSVTVWGAGFADETREERAARINGLISFIGPGGFGTPDDV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS-----ADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGV-DAYHLPFAHKRYLEYLNTL------GTDPESHKRHGRG-EALGNGHALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAKVCAERQGNSQRFTCPYHGWTYDSHGSLIGLP-DKAAYQHA--GQCHPELSLTQVKHA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKC---LGLKEVARV 141
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                     TYPE: amino acids
                                                                                                                                                                                                          NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
                STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Charlotte STATE: No. US20010012886A1th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Drawer 34009
                                                                                                                                    TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BELL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurmukh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL DEATH AND DISEASE RESISTANCE
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                                                                                                                                                                                                                   5718-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
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#1.30

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TOPOLOGY: linear;
; MOLECULE TYPE: protein;
; SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-776-491-19
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                                              RESULT 7
US-09-776-490-20
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US-09-776-491-19
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Best Local S
Matches 33
       Sequence 20, Application US/09776490 Patent No. US20010012886A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 575102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       7.7%;
Local Similarity 94.3%;
les 33; Conservative
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                                                                                                                      1 NVCRHRGKTLVSVEAGNAKGPVCSYHGWGFGSNGK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <URKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Charlotte STATE: No. US20010013135Alth Carolina
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 35 amino acids
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94.3%;
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                                                                                                                                                                                                               Score 185; DB 10; Length 35; Pred. No. 3e-10;
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Pred. No. 3e-10;
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                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                    RESULT 8
US-09-776-491-20
; Sequence 20, Application US/09776491
; Patent No. US20010013135A1
; GENERAL INFORMATION:
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Best Local Similarity 85.,
30; Conservative
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APPLICANT: Briggs,
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MUTTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                            APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESS:
                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                 STREET: P.O. Drawer 34009
CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: (Unknown)
                                                                               STATE: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 35 amino acids
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Gray, John
                                                                               US20010013135Alth Carolina
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85.7%;
                                                                                                                                                                          CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 174; DB 10;
Pred. No. 2.9e-09;
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                                                                                                                                   PARK & GIBSON
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Length 35;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
                                                                                                                                APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
                                                                       APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT IMFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
TELECOMMUNICATION INFORMATION:
                NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                      CITY: Charlotte STATE: No. US20010012886Alth Carolina
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                                                                                                                                                                                                                                                                                                                                                     USA
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85.7%;
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Pred. No. 2.9e-09;
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TOPOLOGY: Ilnear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-776-491-21
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US-09-776-491-21
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 Query Match
Best Local Similarity
Matches 28; Conserv
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Best Local :
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INFORMATION FOR SEQ ID NO: 21:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    ATTORNBY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 571
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 28234
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                               TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Charlotte STATE: No. US20010013135A1th Carolina
                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Drawer 34009
                                                                                                                                                                                       LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BELL, SELTZER, PARK & GIBSON
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TELEX: 575102
 Conservative
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                 7.0%;
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Score 168; DB 10;
Pred. No. 9.8e-09;
3; Mismatches 4
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Pred. No. 9.8e-09;
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                                                                                                                                                                                                                                                                                                                        5718-4
                                                                                             21:
                                   DB 10; Length 35;
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 Indels
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Gaps
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0,
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US-09-776-491-20

TOPOLOGY: linear MOLECULE TYPE: protein

STRANDEDNESS: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid

TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140

NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943 REFERENCE/DOCKET NUMBER: 5718-4

APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:

CLASSIFICATION:

<Unknown>

SOFTWARE: PatentIn F CURRENT APPLICATION DATA:

OPERATING

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001

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US-08-976-063C-4
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Best Local S
Matches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: WORDERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 21-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: BAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 196 4
FILING DATE: 29-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP VECTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alexander Steinbuchel; Horst Priefert; Jurgen TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION: TITLE OF INVENTION: CONIFERYL ALCOHOL, CONIFERYLALDEHYDE, TITLE OF INVENTION: ACID AND THEIR USE NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                      149 DNLM-DLTHETYVHASSIGQKEIDEAPVSTRVEGDTVITSRYMDNVMAPPFWRAALRGNG
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208
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CITY: Tarrytown
STATE: New York
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les 56; Conserv
                                                                                                                                                                                                                                                                                                                                    34 IFARN--WLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                     SFHGFIY---GCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPA 199
                                                                                                            ENFVGDAYHVGWTHASSLR----
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                                                                                                                                                                                                                                                          EAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLG---LKEVARVE 142
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208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 354 amino acids
amino acid
OGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                       4.9%; Score 118.5; DB 1; 23.2%; Pred. No. 0.0067; tive 40; Mismatches 78;
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                                                                                                         SGESIFSS-LAGNAALPP-----EGAG 239
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Of
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US-09-776-491-12
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US-09-776-490-12
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Sequence 12, Application US/09776491
Patent No. US20010013135A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
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Matches 18; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09776490 Patent No. US20010012886A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                      1 NOCRHRGMRICRADAGNAKAPTCSYHGWAYDTAG
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-WAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTATION NUMBER: 32,943
REGISTATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
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CELL DEATH AND DISEASE RESISTANCE IN PLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 35 amino acids
TYPE: amino acid
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TELEX: 575102
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                                                                                                                                        Gray,
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                                                                                                                                        John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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US-09-776-490-14
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NOCKHRGMRICRADAGNAKAPTCSYHGWAYDTAG 34
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
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                                       APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 28234
                                                                                                                                                                                                                                                                           STATE: NO.
                                                                                                                                                                                                                                                                                            CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
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APPLICATION NUMBER: US 08/810,009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 35 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.68;
                                                                                                                                                                                                                                                                           US20010012886Alth Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                    CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110; DB 10; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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RESULT 15
US-09-776-491-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 575102
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        TELEX: 575102
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
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Local Similarity 52.9%;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: FLOOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DO
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Charlotte STATE: No. US20010013135Alth Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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STRANDEDNESS: <UI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EE: BELL, SELTZER, PARK & GIBSON P.O. Drawer 34009
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                                                                                                                                                                                                                                                                                                                                                     919-881-3175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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Pred. No. 0.0017;
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No. of Concession, Name of Street, Square,

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

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Gapop 10.0 , Gapext 0.5
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         GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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         DB
US-09-004-393B-4
US-09-004-393B-2
US-08-810-009-21
US-08-810-009-21
US-08-810-009-12
US-08-810-009-12
US-08-810-009-13
US-08-810-009-13
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US-08-810-009-16
US-08-810-009-16
US-08-810-009-17
US-09-325-932A-57
US-09-134-001C-4800
US-08-810-009-46
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Sequence 20, Appli
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RESULT 2
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; Sequence 2, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
; APPLICANT: Hanson D., Andrew

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Query M Best Lo	Sequence 4, patent No. General INF APPLICANT: APPLICANT: TITLE OF ITILE OF		22200000000000000000000000000000000000
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3%; 4%; 			44441000040444411
tch 9.3%; Score 224; DB 4; Length 446; al Similarity 27.4%; Pred. No. 3.9e-13; 858; Conservative 37; Mismatches 97; Indels 20; G ESGLSCKHLIHGDEELFOHELKTIFARNWLFLHDSLIPAPGDYTAKMGIDEVIVSRON	04393B Bala eotides Encoding Choline ransformed Therewith S/09/004,393B -08 035,147	ALIGNMENTS	US-09-036-987A-6 US-09-370-700-6 US-09-380-009-16 US-09-239-303-2 US-08-348-891A-2 US-08-95-817-2 US-08-570-311-8 US-08-570-311-27 US-08-570-311-27 US-09-341-587-3 US-09-341-587-3 US-09-341-587-3 US-09-149-476-493
Gaps RQN 70 RDG 158 RDG 158 LDK 130 I: LDP 215 LDP 215 RSE 274	Monooxygenase and		Sequence 6, Appli Sequence 16, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 27, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 493, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 439
TYPE: PRT
ORGANIAM: Spinacia oleracea
US-09-004-393B-2
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Sequence 19, App. 1
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CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/035,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                  SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 NYLDSSYHVPYAH 292
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                                                                                                                                          APPLICATION NUMBER: FILING DATE: 04-MAR CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. Dra
CITY: Charlotte
STATE: No. 62114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
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TELEPHONE: 919-001
                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                           ZIP:
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                                                                                  32,943
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                                                                        5718-4
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                                                                                                                                  ; MOLECULE TYPE: protein US-08-810-009-20
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Patent No. 6211437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                 Query Match 7.2%;
Best Local Similarity 85.7%;
Matches 30; Conservative
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                                                                                                                                                                                                                                                    TELEX: 575102
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.V. -
CITY: Charlotte
CTATE: NO. 6211437th Carolina
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1 NVCRHRGKTLVSVEAGNAKGPVCSYHGWGFGSNGK 35
                                   79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 57:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                   STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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1 NVCRHRGKTLYNAEAGNAKGPVCGYHGWGFGSNGK 35
                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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94.38;
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    Mismatches

                                                                                  Score 174; DB 4
Pred. No. 5e-10;
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                                                                    Mismatches
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                                                                                                  DB 4;
                                                                                                Length 35;
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RESULT 5 US-08-810-009-21

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                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                               Sequence 36,
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                   APPLICANT:
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TELECOMMUNICATION INFORMATION: 919-881-3140
                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
                                                                                                                   TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                      APPLICANT:
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                             STREET: 3054 COLUMNA.--
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COUNTRY: UZIP: 27709
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o. 6211437
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6117670
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Gray, John
                                                                                                                                                    van Pee, Karl-He
Kirner, Sabine
Young, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 amino acids
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              USA
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                                                                                                                                                                                 Hammer, Philip E.
van Pee, Karl-Heinz
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80.0%;
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Pred. No. 1.9e-09;
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Sequence 12, Application US/08810009 Patent No. 6211437 GENERAL INFORMATION: APPLICANT: Briggs, Steven P.

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RESULT 7
US-08-810-009-12
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/729,214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 08-JUN-1994
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                                                                               380 DSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSN 428
                                                                                                                                                          290 HMLLAIKKG--DGVVRSAANFILYGLQTWAAAGYDVAIWNSMKAD------GGGAFSKY 340
                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                                                                  207 PPPGQEALARDGAWFGAGIDFHVDRYFGPLGVISRTLGLSMSRMQLHFDGYPG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 IHGDEELFQ-----HELKTIFARNW-LFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGS 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IHQEPERIRQASGVNDLTTQTAASWYVAMRSDALRGKP---VAIKLFGQPLVAWRDGGGR 61
                                                                                                                                                                                                 WTYAIVEKDMPEDLKRRLADSV---QRTTGPAGF----WESDDNDNMETASQNGKKYQSR 379
                                                                                                                                                                                                                                                                                                                                                         SLAGNAALPPE----GAGLQM-TSKYGSGMGVL-------WDGYSGVHSADLV 266
                                                                                                                                                                                                                                                                            PELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEV 326
                                                                                                                                                                                                                                       -----GCIMTVSLD---GDVKYRL----LQCV------TPVDKEETVM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVMERYCSHLGASL------AKGKVVEGCIQCPFHNWRYDSTGACSHVP-----GHS 108
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US-08-810-009-12
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Best Local
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TELEX: 575102
INFORMATION FOR SEQ ID NO:
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NAME: SPINILL W. MUITRY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                       APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
CORRESPONDENCES: 65
CORRESPONDENCE ADDRESS:
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LENGTH: 35 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BELL, SELTZER, PARK & GIBSON
             SOFTWARE: Patentin Relacement APPLICATION DATA: APPLICATION NUMBER: US.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Charlotte
STATE: No. 6211
                                                                                                                                                    COUNTRY: U
ZIP: 28234
                                                                                                                                                                                                       CITY: Charlotte
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                                                                                                                                                                                       No. 6211437th Carolina
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                                                                                                                                                                      USA
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O. Drawer 34009
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04-MAR-1997
V.
04-MAR-1997
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Pred. No. 0.00071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
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US-08-810-009-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13,
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Best Local :
           Query Match
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                                                                                                                                                              TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                MOLECULE TYPE:
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                                                                                                                                                                                   TELEPHONE: 919-881-3175
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                                                                                 TOPOLOGY:
                                                                                               STRANDEDNESS
                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Charlotte
STATE: No. 6211437th Carolina
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                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                              LENGTH:
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Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NQCRHRGMRICRADGGNAKSPTCSYHGWAYDSAG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3, Application US/08810009
                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.O. Drawer 34009
                                                                                                                                 35 amino acids
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                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                               protein
                                                                                                                                                                                                                                                                                                                               04-MAR-1997
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4.5%;
52.9%;
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Pred. No. 0.00088;
Score 108; DB 4; Pred. No. 0.0011;
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                 Length 35;
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Best Local Similarity

Matches

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Conservative

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                                                                                                                                   Sequence 4, Application US/09311626B Patent No. 6399347 GENERAL INFORMATION:
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                                                                                                APPLICANT: Jorgensen, Per Lina
APPLICANT: Schnorr, Kirk
            APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
                                                                 APPLICANT: Andersen, Lene No. 6399347boe APPLICANT: Schulein, Martin
CURRENT APPLICATION NUMBER: US/09/311,626B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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NAME: SPILLIL, W. MULTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57.
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ADDRESSEE: BELL, SELTZER, PARK & GIBSON
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                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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N: 800
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                                                                                                                                                                                                                                                                                                                                        Score 108; DB 4; Pred. No. 0.0011;
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 0608/98
PRIOR FILING DATE: 1998-05-01
                                                                                                                                                                                        APPLICANT: MALSHIOCK
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/084,358
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version
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TYPE: PRT
ORGANISM: Bacillus licheniformis
COMPUTER READABLE FORM:
                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                    COUNTRY:
                                                                  STATE:
                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGVHAGKDVGRGMAADIDPRYEGAEVWANGSLYTAKGV-KIGNTLPSSTNFGIW----- 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRVDRFLAGVAYLDGERPSFVMARGYYTRTVLVAYNFRG---GKLTKLWTFDSDAPGNGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NKEIG-DVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTT-EVWTYAIVE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAGQG-----NHSLSVADVDGDGKDEIIYGAMAVDHDGKG-LYSTGWGHGDAMHTGN 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                      10036-2711
                                                                                    New York
                                                               New York
                                                                                                      1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                 Obara, Kazuhiko
Matsumoto, Akira
                                           USA
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                                                                                                                               Pennie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LDPSRPGLEVFQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiroshi
                                                                                                                                                                                                                               CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
OF ANTIBODY, METHOD AND AGENTS FOR DISCOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
                                                                                                                                                                                               PNEUMONIAE GENE
                                                                                                                                                                                                                 REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                                                                                             Edmonds LLP
                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VYGDAVYPGVVGKSAIG--ETSYRGFY 417
                                                                                                        Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137; Indels 138;
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MEDIUM TYPE:

Floppy disk

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RESULT 13
US-08-809-326A-15
; Sequence 15, Application US/08809326A
Patent No. 6165478
Patent No. 6165478
Patent No. 617010N:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 432 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 WKAPAENFYGDAYHYGWTHASSL------RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
                                                                                                                                                            225
                                                                                                                                                                                                 405 KSAIGETS 412
                                                                                                                                                                                                                                                                                                                                              300 V-----FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGP 354
                                                                                                                                                                                                                                                                                                                                                                                                                       247 GSGMGVLWDGYSGVHSADL------VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     67 GTDDRVTW-----VKSVDEAIAACGDVPEIMVIGGG---RVYEQFLPKAQKLYLTHIDAE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 WNLPAD-----LAWFKRNTLNKPVIMGRHTWESIGRPLPGR-----KNIILSSQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 106010/95 FILING DATE: 28-APR-1995
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                                                                                                                                                              KDKTSSTT 232
                                                                                                                                                                                                                                                                          AGFWESDDNDNME----TASQNGKKYQSRDSD-----LLSNLGFGEDVYGDAVYPGVVG 404
                                                                                                                                                                                                                                                                                                         VEGDTHFPDYEPDDWESVFSEFHDADAQNSHSYEFETLE-----RRILMSISSSSGP 170
                                                                                                                                                                                                                                    -----DNQKNIMSQVLTSTPQGVPQQDKLSGNETKQTQQTRQGKNTEMESDATIAGASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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APPLICATION NUMBER:
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                                                                                                                              195 WKAPAENFVGDAYHVGWTHASSL-----RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
   247 GSGMGVLWDGYSGVHSADL------VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Miller, Charle REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                 22 WNLPAD------LAWFKRNTLNKPVIMGRHTWESIGRPLPGR-----KNIILSSQP 66
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 amino acids
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MATSUMOTO, Akira

CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, DNAS CODING VENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING VENTION: FUSED PROTEINS CONTAINING THE RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA VENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF VENTION: ANTIBODY, METHOD AND REAGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION: OF ANTIBODY AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA VENTION AGENTS FOR 
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                  4.4%; Score 106.5; D
21.4%; Pred. No. 0.13;
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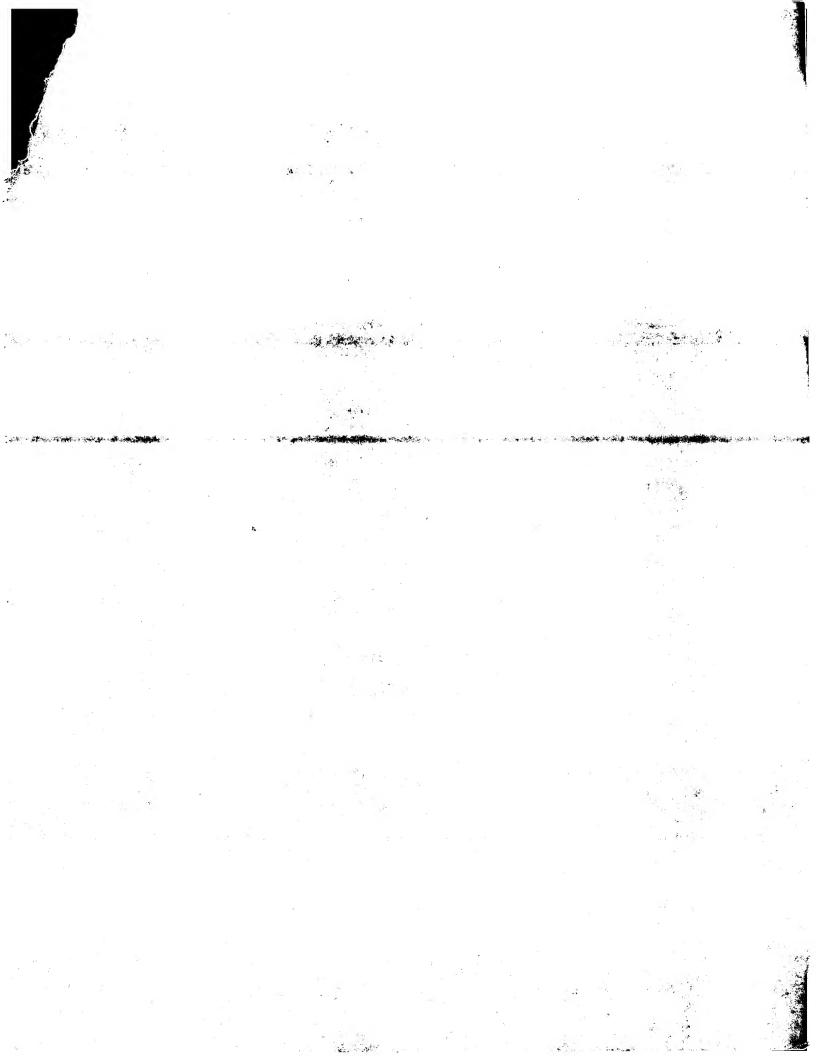
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RESULT 15
US-08-810-009-18
; Sequence 18, Application US/08810009
; Patent No. 6211437
; GENERAL INFORMATION:
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US-08-810-009-9
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Best Local Similarity
Matches 18; Conserv
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Patent No. 6211437
                                                                                                                                                                                                                                                                                                                                                                       TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                   79 NVCRHRGKTLYSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Charlotte
STATE: No. 6211437th Carolina
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                                                                                                                                1 NOCRHRGMRICRSDAGNAKAPTCSYHGWAYDIAGK 35
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N: 800
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Pred. No. 0.0017;
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Search completed: January 27, 2003, 09:04:55 Job time: 11.1667 secs

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-810-009-18
                                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Relacuration DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 04-MAR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                       TELEFAX: 51.
TELEFAX: 575102
SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                    79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
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STREET: P.
1 NSCRHRGALLCPFSKGNQKFHVCRYHGWSYDSSG
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Johal, Gurmukh S.
Gray, John
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BELL, SELTZER, PARK & GIBSON
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                                                                                 4.3%;
52.9%;
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                                                                                Score 104; DB 4;
Pred. No. 0.0027;
                                                                Mismatches
 34
                                                                                              DB 4; Length 35;
                                                                Indels
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                                                            Gaps
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us-09-843-250-34.rspt

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OM protein - protein search, using sw model
                                                               GenCore version 5.1.3 Compugen Ltd.
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Run on: January 27, 2003, 08:54:32; Search time 25.8333 Seconds (without alignments) 3581.232 Million cell updates/sec

Sequence: Title: Perfect score: US-09-843-250-34
2409
1 MNYNNKILYSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_archea:*
sp_bacteria:*
sp_fungi:* sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:*
sp_phage:* sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_invertebrate:*
sp_mammal:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	æ	7	6	U	4	ω	2		No.	Result
1405	1451	1483	1484	1486	1488	1490	1973.5	2022	2051	2071	2187	2191	2206	2290	2330	Score	
58.3	60.2	61.6	61.6	61.7	61.8	61.9	81.9	83.9	85.1	86.0	90.8	91.0	91.6	95.1	96.7	Match Length	OHETV
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Q9euc7 pseudomonas	Q9f5s3 pseudomonas	Q9f5s9 pseudomonas	Q9f5s8 pseudomonas	Q9f5t3 pseudomonas	Q9f5s4 pseudomonas	~	٠.	Q8rtl4 comamonas s	P95564 pseudomonas	Q8vud4 burkholderi	O52382 ralstonia s	Q915d2 comamonas t	Q9zi73 pseudomonas	Q52142 pseudomonas	Q938r9 pseudomonas	Description	

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Q93M39 Q93M41	Q93M40	Q8VUM2	Q8VR21	Q8VUM5	Q9F6B6	Q9WXG8	Q8VR25	Q93NA8	Q8VR22	Q8VR24	Q8VL21	Q8VR23	Q8VUM6	Q9ZHH3	Q9F5S2	Q9F5T7	Q9F5S6	Q9F5T0	Q9F5T1	Q9F5T2	Q9F5T4	Q9F5S7	Q9F5T6	Q9F5S5	Q9ETV3	10	Q9F5T8
Q93m39 Q93m41	Q93m40	Q8vum2	Q8vr2	Q8vum5	Q9f6b6	8pxw6d	Q8vr25	Q93na8	Q8vr22	Q8vr24	Q8v121	Q8vr23	Q8vum6	Q9zhh3	Q9f5s2	Q9f5t7	Q9f5s6	Q9£5ti	Q9f5t1	Q9f5t2	Q9f5t4	Q9f5s7	Q9f5t6	Q9f5s5	Q9etv3	Q9f5t5	Q9f5t8
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ALIGNMENTS

	121 KDLYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	Qy
	61 IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120	DЬ
	61 IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELOSVPFE 120	Qy
	1 MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIFARNWLFLTHDSLIPSPGDYVTAKMG 60	DЬ
	1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60	Qy
0;	Query Match 96.7%; Score 2330; DB 2; Length 449; Best Local Similarity 96.0%; Pred. No. 1.4e-170; Matches 431; Conservative 12; Mismatches 6; Indels 0; Gaps	X E O
	SEQUENCE 449 AA; 49608 MW; 5EFEDBE0282FE812 CRC64;	SQ
	PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.	DR
	Pfam; PF00848; Ring_hydroxyl_A; 1.	DR
	<pre>InterPro; IPR001663; Ring_hydroxyl_A. Pfam: Pr00355: Rieske: 1</pre>	DR DR
	InterPro; IPR001281; Rieske.	DR
	EMBL; AY048759; AAL07262.1;	DR
	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	RL
	Min KH., Ji SH.,	RA
	SEQUENCE FROM N.A.	RP
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	RCBT martn-304.	2 6
	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	88
	Pseudomonas fluorescens.	SO
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	U1-MAR-2002 (TrEMBLrel. 20, Last annotation update)	
	(TrEMBLrel. 19,	P
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                                                                           EMBL; AB004059; BAV
HSSP; P23094; INDO
                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification and characterization of genes encoding polycyclic aromatic hydrocarbon dioxygenase and polycyclic aromatic hydrocarb dihydrodiol dehydrogenase in Pseudomonas putida OUSB2.";
J. Bacteriol. 176:2444-2449(1994).
                                                                                                                                                                                                                       Submitted (JUN-1997)
EMBL; AB004059; BAA20
                                                                                                                                                                                                                                                                                                                     Noboru T., Toshiya I.,
Yue-Wu W., Masao F., Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94209249; PubMed-8157615; TAKIZAWA N., Kaida N., Torigoe S.,
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                              Yue-Wu W., Masao F., Hohzoh K.;
"The molecular analysis of NAH7
Chromosomes of Pseudomonas aeru
                                                                                                                                                                                                                                                                                                                                                              STRAIN-OUS82;
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449 AA; 49361 MW; 80020F54AAB11E8A CRC64;
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01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                    Dioxygenase
SEQUENCE
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Pfam; PF00848; Ring_hydroxyl_A;
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                         EMBL; AF039533; AAD02136.1;
HSSP; P23094; INDO.
                                                                                                                                                                                              chromosomally encoded naphthalene-degradation upper pathway Pseudomonas stutzeri AN10.";
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MEDLINE-99365311; PubMed=10433976;
                                                                                           PROSITE;
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InterPro; IPR001663; Ring_hydroxyl_A.
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"Genetic characterization and evolutionary
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                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                        InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSTIE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moser R., Stahl U.;
"Insights into the genetic diversity of initial degrading bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Polyaromatic hydrocarbon dioxygenase large subunit.
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl. Microbiol. Biotechnol. EMBL; AF252550; AAF72976.1; -HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comamonas testosteroni (P: Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9L5D2
                                                                                                                                                                                                                                                                                                          Dioxygenase
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                          IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                447 AA;
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                49548 MW;
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88.9%;
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                                                                                                                                                                          Score 2191; DB 2;
Pred. No. 6.7e-160;
7; Mismatches 21;
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           Query Match
Best Local (
 Matches
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O52382;
O1-JUN-1998 (TrEMBLrel. 06, C
O1-JUN-1998 (TrEMBLrel. 10, L
O1-DEC-2001 (TrEMBLrel. 19, L
Naphthalene 1,2 dioxygenase 1
                                                                                                                                               Zhou N.Y., Fuenmayor S.L., Williams P.A.; "nag genes of ralstonia (Formerly pseudomonas) enzymes for gentisate catabolism.";
J. Bacteriol. 183:700-708(2001).
EMBL; AF036940; AAD12810.1; -.
HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                       MEDLINE=98233751; PubMed=9573207;
Fuenmayor S.L., Wild M., Boyes A.L., Williams
"A gene cluster encoding steps in conversion c
gentisate in Pseudomonas sp. strain U2.";
J. Bacteriol. 180:2522-2530(1998).
                                                                                              Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                 SEQUENCE
                                                              Dioxygenase;
                                                                       PRINTS; PR00090; RING_HYDROXYL_ALPHA; PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                     InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                        STRAIN-U2
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                                                                                                                                                                                                                          MEDLINE=20576173;
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 Conservative
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                                                 49570 MW;
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89.1%;
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large oxygenase compc
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            Score 2187;
Pred. No. 1.
                                                 4553AAF4B4410ED0 CRC64;
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 Mismatches
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01-MAY-1997
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                                                                                                                                 EMBL; U49504; AAB40383.1; -.
HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001281; Rieske.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00909; RNOBIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
SEQUENCE 447 AA; 49485 MW; 1CB0E223E528E3BD CRC64;
                                                                                                                                                                                                                                      dioxygenase from Pseudomonas sp. Gene 181:57-61(1996).
                                                                                                                                                                                                                                                                                                                                                             NTDAC
                                                                                                                                                                                                                                                           MEDLINE=97128768; PubMed=8973308; Parales J.V., Kumar A., Parales R.E., "Cloning and sequencing of the genes"
                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria.
NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
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                                                       1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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VDEVIVSRQNDGSVRAFLNVCRHRGKTLVHTEAGNAKGFVCGYHGWGYGSNGELQSVPFE
          IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                            MSYQN--LVSEAGLTQKLLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVTAKMG
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pathway

Microbiol. 173:86-90(2000).

Johnson G.R., Jain R.K., Spain J.C.; "Properties of the trihydroxytoluene oxygenase cepacia R34: an extradiol dioxygenase from the

from Burkholderia
2,4-dinitrotoluene

MEDLINE=20254695; PubMed=10795678;

SEQUENCE FROM N.A.

Qy

DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY

420

358 360 298

FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES QMTSKYGSGMGVLWDGYSGVHSADLVPEMMAFGGAKQEKLAKEIGDVRARIYRSHLNCTV QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV

FPNNSTLTCSGVFKVWNPIDENTTEVWTYAIVEKDMPEDLKRRLADAVQRTFGPAGFWES

DDNDNMETESQNAKKYQSSNSDLIANLGFGKDYYGDECYPGVVAKSAIGETSYRGFYRAY

밁 Qy В 204 Вþ δδ В QΥ В Ş В

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240

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IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120

VDEVIVSRQNDGSVRAFLNVCRHRGKTLVHAEAGNAKGFVCSYHGWGFGSNGELQSVPFE

118

58

181 119 121

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QAHVSSSNWAEFEHASSTWHTELTKTTDR 449

QAHISSSNWAEFENTSRNWHTELTKTTDR

447

359 361 299 301 239 241

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Q8VUD4; Q8VUD4

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DntAc. Burkholderia

cepacia (Pseudomonas cepacia).

beta

subdivision;

Burkholderia

group;

Bacteria; Proteobacteria; Burkholderia.

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MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG

Query Match Best Local S Matches 375

al Similarity 375; Conserv

Conservative

38;

Score 2071; D Pred. No. 1.1e 38; Mismatches

DB 2; .1e-150;

2;

Gaps

60

CRC64; Length Indels

86.0%;

Pfam; PF00355; Rieske; 1.

Pfam; PF00848; Ring_hydroxyl_A; 1.

PRINTS; PR00090; RNGDIOXGNASE.

PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.

SEQUENCE 447 AA; 49468 MW; ZA5BF8558320275C (

Johnson G.R., Jain R.K., Spain J.C.; "Origins of the 2,4-dinitrotoluene pathway."; "Submitted (JUN-2001) to the EMBL/GenBank/DDBJ EMBL; AF169302; AAL50021.1; -.

databases

STRAIN-R34; SEQUENCE FROM

N.A.

InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.

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Q8RTL4;
01-JUN-2002 (TrE)
01-JUN-2002 (TrE)
01-JUN-2002 (TrE)
01-JUN-2002 (TrE)
0xygenase-alpha 1
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Appl. Environ. Microbiol. 68:634-641(2002).
EMBL; AF379638; AAL76202.1: -
SEQUENCE 447 AA; 49556 MW; 4CA961F99A371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21681044; pubMed=11823201; Lessner D.J., Johnson G.R., Parales R.E., Spain J.C., "Molecular Characterization and Substrate Specificity Dioxygenase from Commamonas sp. Strain JS765.";
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Bacteria; Proteobacteria;
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                                                                                    KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
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                       QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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QMTSKYGSGMGVFWGYYSGNFSADMIPDLMAFGAAKQEKLAKEIGDVRARIYRSFLNGTI
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J. Bacteriol. 178:4926-4934(1996).
EMBL; U62430; AAB09766.1; -.
HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Dfan. DE00355. Biolog. 1
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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"2,4-Dinitrotoluene dioxygenase from Burkholderia
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DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                         FPNNCFLTGAGVFKVFNPIDENTTEAWTYAIVEKDMPEDLKRRLADAAQRSTGPAGYWES
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Ferrero M.A., Lalucat J., Bosch R.;

T "Coexistence of two naphthalene dioxygenase genes (nahAc) in Pseudomonas strains from West Mediterranean Sea.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. REMBL; AF306438; AAG25698.1; -. REMBL; AF306438; AAG25692.1; -. REMBL; AF306432; AAG25692.1; -. REMBL; AF306436; AAG25692.1; -. REMBL; AAG25692.1; -. REMBL; AAG25692.1; AAG256
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"Coexistence of two naphthalene dioxygenase genes (na pseudomonas strains from West Mediterranean Sea.";

L Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databas REMBL; AF306440, AAA25700.1;

R EMBL; AF306440, AAA25700.1;

R EMBL; AF306481, INDO.

R InterPro; IPR001281; Rieske.

InterPro; IPR001281; Rieske.

InterPro; IPR00155; Rieske; 1.

R InterPro; IPR00155; Rieske; 1.

R Pfam; PF00355; Rieske; 1.

R Pfam; PF00348; Ring_hydroxyl_A; 1.

R Pfam; PF00348; Ring_hydroxyl_A; 1.
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  Pseudomonas strains Submitted (SEP-2000)
                      Ferrero M.A., Lalucat J., Bosch R.; "Coexistence of two naphthalene dioxygenase Pseudomonas strains from West Mediterranean
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Best 1
Query Match
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Q9F5S8;
01-MAR-2001
01-MAR-2001
                                                               NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                     Ferrero M.A., Lalucat J., Bosch R.; "Coexistence of two naphthalene dioxygenase genes (nahAc) pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-200) to the EMBL/GenBank/DDBJ databases. EMBL; AF306434; AAG25694.1; -
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                                                                                                                            Dioxygenase.
                                                                                                                                               PROSITE;
                                                                                                                                                                   Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                       InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=139773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Naphthalene
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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hes 276;
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                                                                                                                                               PS00570; RING_HYDROXYL_ALPHA;
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277
277 AA;
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(TrEMBLrel. 19, Last annotation update)
dioxygenase iron sulfur protein (Fragment).
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30064 MW;
61.6%;
99.6%;
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99.6%;
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Score 1484; DB 2
Pred. No. 6e-106;
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Pred. No. 4.2e-106;
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01-MAR-2001
01-DEC-2001
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NON_TER
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SEQUENCE 27
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00099; RNGDIOXNNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA
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                                                       HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
                                                                                                                               SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                                                                                                  TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ
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EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH
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277
29995 MW;
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16, Last
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Search completed: January 27, Job time: 27.8333 secs
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01-MAR-2001
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InterPro; IPRO01663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSTIE; PS00570; RING_HYDROXYL_ALPHA;
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NCBI_TaxID=303;
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                                                                                        LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 332
                                                                                                                                                                                   HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP 235
                                                                                                                                                                                                                                                                                                                                                                                                SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKMGIDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQ
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
dioxygenase iron sulfur protein 1 (Fragment).
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 08:47:32; Search time 7.16667 Seconds (without alignments) 2598.540 Million cell updates/sec

Title:
Perfect score:
Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

US-09-843-250-34
2409
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P11491 :	Q04610 l	Q12558 a	070472 1	P35972 r	059650	Q9bzf1 l					P51851 I	
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ALIGNMENTS

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SPECIES-P.Dutida; STRAIN-NCIB 9816; Parales J.V., Parales R.E., Kumar A., Gibson D.T.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. SIRAIN-CL8; STRAIN-CL8; MEDLINE-94042852; Pubmed-8226631; Denome S.A., Stanley D.C., Olson E.S., Young K.D.; "Metabolism of dibenzothiophene and naphthalene in Pseudomonas strains: complete DNA sequence of an upper naphthalene catabolic pathway."; J. Bacteriol. 175:6890-6901(1993). SEQUENCE FROM N.A. SPECIES-P.Dutida; STRAIN-G7 / ATCC 17485; PLASMID-NAH7; SEQUENCE FROM M.J., Osslund T.D., Saunders R., Ensley B.D., Suggs S., MEDLINE-9325227; Pubmed-8486285; Simon M.J., Osslund T.D., Saunders R., Ensley B.D., Suggs S., HARCOURT A.A., Suen WC., Cruden D.L., Gibson D.T., Zylstra G.J.; "Sequences of genes encoding naphthalene dioxygenase in Pseudomonas putida strains G7 and NCIB 9816-4."; Gene 127:31-37(1993). [5] SEQUENCE FROM N.A. SPECIES-P.Dutida; STRAIN-BS202; PLASMID-NPL1; Bezborodnikov S.G., Boronin A.M., Tiedje J.M.; "Nucleotide sequences of genes encoding an upper pathway of naphthalene metabolism of NPL1 plasmid from Pseudomonas putida strain BS202."; SLUmitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.	LT 1 PSEPP PSEPP PSTP PSTP PSTP PSTP PSTP P

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EMBL; M23914; AAB47591.1; -. EMBL; U49496; AAA52141.1; -. EMBL; M60405; AAA16125.1; -. EMBL; M83949; AAA25902.1; -. EMBL; AF010471; AAB62707.1; -. EMBL; AF010471; AAB61373.1; -. PIR; J30071; J30071, J30071; PIR; B49343; B49343. PDB; 1NDO; 23-MAR-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1,2-dinydronaphthalene-1,2-din1 + NAD(+).

-i: COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

-!- PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHIOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO 1-HYDROXY-2-WAPTHOIC ACID AND THE METABOLISM OF DET IS LIMITED TO OXIDATION OF THE AROMATIC RING.

-!- SUBUNIT: NAPHTHALENE DIOXYGENASE (MO) MULTICOMPONENT ENZYME SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT IS COMPOSED OF FREEDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS COMPOSED OF AN HEXAMER OF THREE LARGE ALPHA SUBUNITS (NDOB) AND THREE SMALL BETA SUBUNITS (NDOC).

-!- SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                       Dioxygenase;
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1NDO; 23-MAR-99.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramaswamy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-P.putida; STRAIN-NCIB 981
MEDLINE-98298434; PubMed-9634695;
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00090; RNGDIOXGNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of an aromatic-ring-hydroxylating dioxygenase-naphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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ructure 6:571-586(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATI
BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CIS-
NAPHTHALENE DIHYDRODIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
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                                                                                                                                                                      NAD;
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007824;
15-DEC-1998
15-DEC-1998
15-JUN-2002
Naphthalene
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ-!- FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGE WILTICOMPONENT ENZYME SYSTEM WHICH CATALYZ BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTH NAPHTHALENE DIHYDRODIOL.
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1,2-dioxygenase alpha subunit (EC
nase ISP alpha).
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InterPro; IPR001663; Ring_hydroxyl_A.
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COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES

CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF

DIBENZOTHIOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHREN

1-HYDROXY-2-NAPTHOLC ACID AND THE METABOLISM OF DBT IS LIMITE

OXIDATION OF THE AROMATIC RING.

SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT AND AN IRON SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS
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                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                               FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES
                                                                                                                     QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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PF00848; Ring_hydroxyl_A; 1.
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RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q51494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                                                                                                                                                                           Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                      InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                  EMBL; D84146; HSSP; P23094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The molecular analysis of an NAH7-type gene cluster, pah, located the chromosome of Pseudomonas aeruginosa PaK1."; the chromosome of Pseudomonas aeruginosa PaK1."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Naphthalene 1,2-dioxygenase alpha subunit (EC
1,2-dioxygenase ISP alpha).
                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                     PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDOB OR PAHA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kiyohara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PaK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
                                                                                                                                                                 Aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAPHTHALENE DIHYDRODIOL.

NAPHTHALENE DIHYDRODIOL.

CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1,2 dihydronaphthalene-1,2-diol + NAD(+).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHIOPHENE (DBT) AND PHENANTHENE. CONVERTS PHENANTHI 1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DBT IS LIMIOXIDATION OF THE AROMATIC RING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NDOC).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT AND AN IRON SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS COMPOSED OF A LARGE ALPHA SUBUNIT (NDOB) AND A SMALL BETA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAHVSSSNWAEFEDASSTWHTELTKTTDR 449
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                                                                                                                                                                 PS00570; RING hydrocarbons
  NAD.
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                                                                                                                                                                                         RING_HYDROXYL_ALPHA;
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                                                                                                                                                                 catabolism;
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY).
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                                SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         HCAE_ECOLI STANDARD; PRT; 453 AA.

047139; P77590; P78203;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

3-phenylpropionate dioxygenase alpha subunit (EC 1.1)

(Digoxigenin alpha subunit).

HCAE OR PHDC1 OR HCAA OR HCAA1 OR DIGA OR B2538 OR 1

Escherichia coli, and

Escherichia coli 0157:H7.
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Best Local S
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                                                                            Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D Mau B., Shao Y.;
                                                                                                                          SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloc
Riley M., Collado-Vides J., Glasner
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                                                                                                                                                                                                                                                                                                            STRAIN=K12;
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  SEQUENCE
                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                          Turlin
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                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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nes 403; Conserv
                                       complete genome sequenc
nce 277:1453-1474(1997).
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  FROM
                                                                                                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                , Gasser F., Biville F.; (SEP-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                     Gasser F.,
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Pred. No. 1e-1
23; Mismatches
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RON (BY SIMILARITY).
35A189136722A21C CR
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                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIGA OR B2538 OR Z3809 OR ECS3404
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23;
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                                                                coli K-12.
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Yhew G.F.
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                                                                                                          D.J.,
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RC STRAIN-0157:H7 / RIMD 0509952;

RX MEDLINE-21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Kihara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genomic comparison with a laboratory strain K-12.";

RT "Complete genomic comparison with a laboratory strain K-12.";

RT "O157:H7 and genomic comparison with a laboratory strain K-12.";

RT DIAA Res 8:11-22(2001).

CC -I- FUNCTION: PART OF MULTICOMPONENT 3-PHENYLPROPIONATE DIOXYGENASE.

CC CONVERTS 3-PHENYLPROPIONIC ACID (PP) INTO CIS-3-(3-CARBOXYETHYL)-

CC -I- FUNCTION: PART OF MULTICOMPONENT 3-PHENYLPROPIOLO.

CC -I- CYPLOHEXADIENE-1, 2-DIOL (PP-DINYDRODIOL).

CC -I- CYPLOHEXADIENE-1, 2-DIOL (PP-DINYDRODIOL).

CC -I- COPACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

-I- PATHWAY: 3-PHENYLPROPIONIC acid catabolism.

CC -I- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: THE

TWO SUBUNITS: OF THE HYDROXYLASE COMPONENT (HCAE AND HCAF). A

FERREDOXIN (HCAC) AND A FERREDOXIN REDUCTASE (HCAD).

C-I- SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING

DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."

Nature 409:529-533(2001).
                                                                                                    InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Ison Itoh T., Kinura S., Kitagawa M., Makino K., Miki T., Miks Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivas Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K
                                                                                                                                                                                                                   EMBL; AP002562; BAE HSSP; P23094; INDO.
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MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                  sWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content
                                                                                                                                                                                                                                AE005484; AAG57651.1;
AP002562; BAB36827.1;
                                                                                                                                                                                                                                                                      D90883; BAA16433.1; -. D90884; BAA16441.1; -.
                                                                                                                                                                                                                                                                                                        Z37966; CAA86018.1; -. AE000340; AAC75591.1; -
                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long d and this statement is not removed s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                              EG13456; hcaE.
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, Mitsuhashi N.,
imoto H.,
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no
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Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; NAD; Complete proteome.

METAL 85 85 ERON-SULFUR (2FE-2S)

METAL 87 87 IRON-SULFUR (2FE-2S)

METAL 105 105 IRON-SULFUR (2FE-2S)

PS00570; RING_HYDROXYL_ALPHA; 1.

Iron-sulfur; Iron;

(BY (BY)

Y SIMILARITY). Y SIMILARITY). Y SIMILARITY).

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BED1_PSEPP
ID BEID1
AC Q07944
DT 01-NOV
DT 01-NOV
DT 16-OCT
DE BERCEN
GN BEECL.
OS PSeudo
OG Plasmi
OC PSeudo
OX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RA TAN H.
CC -!- CA
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Best Local Sim
Matches 165;
                                                                                                                                                                                                                                                                      BEDI_PSEPU STANDARD;
Q07944;
01-NOV-1995 (Rel. 32, Cre
01-NOV-1995 (Rel. 32, Las
16-OCT-2001 (Rel. 40, Las
Benzene 1,2-dioxygenase a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                           Tan H.-M., Tang H.-Y., Joannou C., Abdel-Wahab N.H., Mason J.R.; "The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenase are unusual in codon usage and low in G+C content."; Gene 130:33-39(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
                                                                                                                                                                                                                          Plasmid PHMT112
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                                                                                                                                       STRAIN-ML2
                                                                                                                                                                                                                                           Pseudomonas putida.
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                                                                                                                        MEDLINE=93345820;
                                                                                                                                                                                NCBI_TaxID=303;
                                                                                                                                                    EQUENCE FROM N.A., AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          421
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CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-dihydrobenzene-1,2-diol + NAD(+).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
PATHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVESYKGLIFGNWDTSAPGLRDYLGDIAWYLDGMLDRREGGTEIVGGVQKWVINCNWKFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                          ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
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                                                                                                                                                                                                             Proteobacteria;
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                                                                                                                      PubMed=8344526;
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Last annotation update)
se alpha subunit (EC 1.14.12.3).
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4; Mismatches 174; Indels
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V ->
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YQRWADLLSSESWQEVLDKTAAYQQEVMK -> ATAPATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON-SULFUR (2FE-2S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02535BF5F47643FD CRC64;
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Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF148496; AAA17758.1; HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dioxygenase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                          AHVSSSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
KMMTSPDW
                                                                                     DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ 421
                                                                                                                   PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
                                                                                                                                      PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWESD
                                                                                                                                                                               WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF
                                                                                                                                                                                                           WDGY-SGVHSAD-----LVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVF
                                                                                                                                                                                                                                                           WKAPAENFYGDAYHYGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
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                                                                                                                                                                                                                                                                                                                                                                             VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                          IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                        DGENWVEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
                                                                                                                                                                                                                                         WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP------KFGKQYRAS
                                                                                                                                                                                                                                                                                                                               -- VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                                                                                                                                                                                                              QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA-----CLDKKEWS
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                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04996; AAA26005.1; PIR; A36516; A36516.
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01-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zylstra G.J., Gibson D.T.;
"Toluene degradation by Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zylstra G.J., Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89359301; PubMed=2670929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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                                                                                                                             VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
VLWDGYSGVHSADLVPELMAF---GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                      WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                            WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                  PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                         --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                                             IYTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLN
                                                                                                                                                                                    IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                                                PF00355; Rieske; 1.
PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
                                                                                                                                                                                                                       Pred.
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(BY SIMILARITY)
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(EC 1.14.12.-).
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                                                                                                                use by modified
                                                                                                                                                                                  This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                    Haddock J.D., Gibson D.T.;
J. Bacteriol. 178:2158-2158(1996).
J. CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).

-i- COFACTOR: Binds 1 2Fe-25 cluster and 1 1ron and 1
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                   EMBL; M86348; AAB63425
                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and characterization biphenyl 2,3-dioxygenase from Pseuc J. Bacteriol. 177:5834-5839(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-LB400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequencing and transcriptional mapping of the encoding biphenyl dioxygenase, a multicomponent polychlorinated-biphenyl-degrading enzyme in Pseudomonas s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92234948; PubMed=1569021;
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Burkholderia
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15-JUN-2002 (Rel. 41, Last
15-JUN-2002 (Rel. 41, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96011369;    PubMed=7592331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-10,
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                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                             SUBUNIT: Heterohexamer consisting of three BphA subunit BphE subunits. A ferredoxin (BphF) and a ferredoxin red (BphG) must be present to obtain activity.

SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit PATHWAY: Biphenyl-polychlorinated biphenyl degradation pathway
                                                                                                                                                                                                                                                            DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                               first step.
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                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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Q46372;
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15-JUN-2002 (Rel. 41, Last a:
15-JUN-2002 (Rel. 41, Last a:
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Bacteria; Proteobacteria;
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
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32.9%;
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PROSITE; PS00570; RING_HYDROXYL_ALPHA;
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PATHWAY: Biphenyl-polychlorinated biphenyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEV-
                  FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGETSYR
                                                                 --TVFPTCSFLPGINTIRTWHPRGPNEVEVWAFVLVDADAPEDIKEEFRLQNIRTFNAGG
                                                                                                          NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAG
                                                                                                                                                                              CNWKFAAEQFCSDMYHAGTMSHLSGVLAG----
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                                                                                                                                                    NQFRSAWGGHGAGWFINDSSILLSVVGPKITQYWTQGPAAEKAARRVPQLPILDMFGQHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON-SULFUR (2FE-2S) (IIRON-SULFUR (2FE-2S) (IIRON-SULFUR (2FE-2S) (IIRON-SULFUR (2FE-2S) (IIRON (BY SIMILARITY).
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Pred. No. 7.2e-41;
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                                 Query Match
Best Local S
Matches 147
                                                                                METAL
SEQUENCE
                                                                                                                                                   METAL
                                                                                                                                                                                               Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taira K., Hirose J., Hayashida S., Furukawa K.;

"Analysis of bph operon from the polychlorinated biphenyl-degrading strain of Pseudomonas pseudoalcaligenes KF707.";

J. Biol. Chem. 267:4844-4853(1992).

-i- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R, 3S)-3-phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).

-i- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit (By
                                                                                                                                                                                                                                                        EMBL; M83673; AAA25743.1; -. HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BPHA_PSEPS
Q52028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Biphenyl dioxygenase alpha subunit (EC 1.14
                                                                                                                                                                Dioxygenase;
                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                              InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas pseudoalcaligenes
Bacteria; Proteobacteria; gam
                                                                                                                                                                         PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
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PHA OR BPHAl.
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         11 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Heterohexamer consisting of three BphA subunits and 1 BphE subunits. A ferredoxin (BphF) and a ferredoxin reductase (BphG) must be present to obtain activity (By similarity). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
PATHWAY: Biphenyl-polychlorinated biphenyl degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                           first step
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                                  al Similarity
147; Conser
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458
                                   Conservative
                                                                                                                                                                NAD.
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25.5%;
33.1%;
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                                   70;
                                                                                         IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON (BY SIMILARITY).
IRON (BY SIMILARITY)
                                              Score 615;
                                 Pred. No. 7.2e
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ion update)
(EC 1.14.12.18)
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                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                            .2e-41;
                                                         DB 1;
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                                   183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonadaceae
=
                                                        Length
                                                                                CRC64;
                                                                                                                (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                  Indels
                                                                                                                                                                          Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Biphenyl 2,3-
                                                         458
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                                 Gaps
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01-AUG-1988
01-NOV-1988
15-JUL-1999
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1. CAMALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-
dihydrobenzene-1,2-diol + NAD(+).

dihydrobenzene-1,2-diol + NAD(+).

1. COPACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

1. PARHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.

1. PARHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO PROTEIN
EMBL; M17904; AAA25735.1; PIR; A29830; A29830.
                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
between the Swiss Institute of Bioinformatics and the Ew
the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             benzene oxidation enzymes of Pseudomonas putida.", J. Bacteriol. 169.5174-5179(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Benzene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Irie S., Doi S., Yorifuji T., Takagi M., Yano
"Nucleotide sequencing and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                         SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS: TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BNZA AND BNZB), FERREDOXIN (BNZC) AND A FERREDOXIN REDUCTASE (BNZD).
                                                                                                                                                                                                                                                                                                       FERREDOXIN (BNZC)
SIMILARITY: BELOW
                                                                                                                                                                                                                                                                             DIOXYGENASE ALPHA SUBUNIT FAMILY.
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                                                                          an email to license@isb-sib.ch).
                                                                                                    requires
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(Rel. 09,
(Rel. 38,
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                                                                                            tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Last annotation
se alpha subunit
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(EC 1.14.12.3) (P1 subunit).
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Best Local S
Matches 143
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Q52438;
Q52438;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12.18) (Biphenyl
SEQUENCE FROM N.A.

MEDLINE-94324977; PubMed-8048958;
Fukuda M., Yasukouchi Y., Kikuchi Y., Nagat
Horiuchi H., Takagi M., Yano K.;

"Identification of the bphA and bphB genes
KKS102 involved in degradation of biphenyl
                                                                                               Bacteria; Proteobacteria
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                                                                                    NCBI_TaxID=307
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IPR001663; Ring_hydroxyl_A.
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  polychlorinated
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Biochem. Bio
-!- CATALYTI
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D17319; BAA04137.1; -. HSSP; P23094; INDO.
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Aromatic hydrocarbons catabolism; Oxidore
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SUBUNIT: Heterohexamer consisting of 3 BphAl subunits and 3 BphA2 subunits. A ferredoxin (BphA3) and a ferredoxin reductase (BphA4) must be present to obtain activity (By similarity).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. Biophys. Res. Commun. 202:850-856(1994).
CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R, phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
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SYRGFYRAYQAHVSSSNW
                                                                                             PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGET
                                                                                                                                                                                                                                                                                                       SGMGVLWDGYSGVHSADLVPELMAFGGAK-----QERLNKEIGDVRAR-IYRSHL
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                                                  AGGTFEQDDGENWVEIQRGLRGHKAKSAPLCAQMGLNVPNKSNPDFP---
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147; Conserv
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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nes 174;
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RESULT 12

XYLX_PSEPU
ID XYLX_P
AC P23099
DT 01-NOV
DT 01-NOV
DT 15-DEC
DE TOLLASMI
OC P30090
OC PSEUDEN
RA NEIGLE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-92155191; PubMed-1740120;
Hartnett C., Ornston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00570; RING_HYDROXYL_ALPHA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Acinetobacter calcoaceticus chromosomal bend gene are the short-chain alcohol dehydrogenase superfamily.";
I. J. Biochem. 204:113-120(1992).
COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
PATHWAY: DEGRADATION OF BENZOATE AND TOLUATE TO CATECHOL.
SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEIL
TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (XYLX AND XYLY)
ELECTRON TRANSFER COMPONENT (XYLZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S23482; S23482.
HRGATLCRFRSGNKATHTCSFHGWTFSNSGKLLKVKDPKGAGYPDSFD--CDGSHDLKKV
                                HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKKCLG---LKEV
                                                                                           DPRLFDLEMKHIFEGNWIYLAHESQIPEKNDYYTTQMGRQPIFITRNKDGELNAFVNACS
                                                                                                                      DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
                                                                                                                                                                                             105;
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                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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20, Last sequence update)
37, Last annotation update)
genase alpha subunit (EC 1.14.12.-).
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31.2%;
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY)
IRON (BY SIMILARITY)
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Pred. No. 8.
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           Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDTOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          for benzoate 1,2-dioxygenase reveal
multicomponent oxygenases.";
J. Bacteriol. 173:5385-5395(1991).
 Aromatic hydrocarbons
                                                           InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                        EMBL; AF009224; AAC46436.2; PIR; S23477; S23477.
                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                               entities
                                                                                                                                                          modified and this statement
                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 84; 103-104;
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MEDLINE=91358314; PubMed=1885518;
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Nucleotide sequences of the Acinetobacter calcoaceticus benABC
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                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on i
                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                              COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON PATHMAY: DEGRADATION PATHMAY LEADING FROM BENZOATE I SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE F TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BENA AND
                                                                                                                                                                                                                                         DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                    AN ELECTRON TRANSFER COMPONENT (BENC).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
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                                                                                                                                            license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                      institutions as long
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catabolism; Oxidoreductase; Iron-sulfur;
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Best Local S
Matches 128
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative dioxygenase alpha subunit yeaW (EC 1
YEAW OR B1802 OR EC82511.
                                                                     Blattner F.R., Plunkett G. III, Bloch C.A., Per Riley M., Collado-Vides J., Glasner J.D., Rode Gregor J., Davis N.W., Kirkpatrick H.A., Goeder
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STRAIN=K12;
             SEQUENCE
                                      Science
                                               "The
                                                                                                             STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                   Escherichia coli, and Escherichia coli 0157:H7.
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                                   complete genome sequence nce 277:1453-1474(1997).
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                                                             Shao Y.;
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27.7%;
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3; Mismatches
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                                                                                                                                                                                       subdivision;
                                                Escherichia coli K-12.";
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                                                                      Goeden M.A., Rose
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                                                                                  Perna N.T., Burlode C.K., Mayhew
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-!- SUBUN
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"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."

"Asture 409:529-533(2001).
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Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T. Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
Yamamoto Y., Horiuchi T.;
A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                   METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE005403; AAG56791.1; -. EMBL; AP002558; BAB35934.1; -. EcoGene; EG13509; yeaW.
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MEDLINE=21156231; PubMed=11258796;
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MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00355;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001281; Rieske
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       23
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COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN SUBUNIT: PROBABLE HETERODIMER OF YEAW AND YEAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through the the Swiss Institute of Bioinformatics and the ENEUROPEAN BIOINFORMATICS INSTITUTE. There are no restricted the statement of the swind of the swind                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                    Complete
    DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE000274; AAC74872.1; -.
D90823; BAA15597.1; ALT_INIT.
D90824; BAA15606.1; ALT_INIT.
                                                                         Similarity
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7:Н7
                                                     Conservative
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                                                     53;
                                                   Score 246; DE
Pred. No. 5.3e
53; Mismatches
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IRON-SULFUR (2FE-2S)
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                                                   DB 1; 15.3e-12; nes 127;
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RESULT 15
CHMO_AMATR
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Amaranthaceae; Amaranthus.

MCBI_TaxID=29722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                      Meng Y.L., Wang Y.M., Zhang B., Nii N.;
"Isolation of a choline monooxygenase cDNA clone from Amaranthus tricolor and its expressions under stress conditions.";
Cell Res. 11:187-193(2001).
"Indicate the first step of the osmoprotectant glycine". PUNCTION: Catalyzes the first step of the osmoprotectant glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 betaine synthesis.
-!- CATALYTIC ACTIVITY: Choline + 2 reduced ferredoxin + O(2) = betaine aldehyde + 2 oxidized ferredoxin + H(2)O.
-!- COFACTOR: Magnesium. Probably binds a 2Fe-2S group and an in
                                                  Pfam; PF00355; Rieske; 1.
Monooxygenase; Oxidoreductase; Chloroplast; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choline monooxygenase, chloroplast precursor (EC 1.14.15.7).
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                                                                                                                   InterPro;
                                                                                                                                           EMBL; AF290974; AAK82768.1; -.
                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21520075; PubMed=11642403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGTDAAFHGFW-----LWPCTM-------LNVT--PIKGMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRGKTLVSVEAGNAKGFV-CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESFHGFTYGCFDQEAPPLMDYL-GDAAWYLEPM----FKHSGGLELVGPPGKVVIKANW 195
                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                IPR001281; Rieske.
  Transit peptide.
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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CHLOROPLAST (BY SIMILARITY).
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                                                            KKCLGLKEVARVESFHGFIYGCFDQEAPP-----LMDYLGDAAWYLEPMFKHS--GGLEL 182
                                                                                  GQGKVHAFHNVCTHRA-SILACGTGKKSCFVCPYHGWVFGLDGSLMKATKTEN---QVFD
                                                                                                                             AEDGFTPPSTWYTDPSLYSHELDRIFSKGWQVAGYSDQIKEPNQYFTGSLGNVEYLVCRD 153
                   VGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
IN-RSEFPMESNWKVFCDNYLDSAYHVPYAH
                                                                                                       NDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLN
                                        PKELGLVTL-KVAIWGPFVLISLDRSGSEGTEDVGKEWIGSCA---EEVKKHAFDPSLQF
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IRON-SULFUR (2FE-2S) (E
IRON-SULFUR (2FE-2S) (E
IRON-SULFUR (2FE-2S) (E
IRON-SULFUR (2FE-2S) (E
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Search completed: January 27, Job time: 8.33333 secs 2003, 08:59:40

GenCore version 5.1.3 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 08:55:37; Search time 13.1667 Seconds (without alignments) 3278.305 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-843-250-34 2409

Scoring table:

1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2	200	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	_U	4	ω	2	1		Result
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aromatic oxygenase	biphenyl dioxygena	probable ring-hydr	anthranilate dioxy	e ben	\vdash		benzoate 1,2-dioxy		l d	•	TD.			_	\vdash		\vdash	C	_	_		terminal oxygenase	naphthalene dioxyg		α			naphthalene dioxyg	Describeron	

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186	214.5	223	224	233.5	246	246	246	249.5	263	269.5	283	287	291	311.5	311.5
7.7	8.9	9.3	9.3	9.7	10.2	10.2	10.2	10.4	10.9	11.2	11.7	11.9	12.1	12.9	12.9
426	186	439	446	382	374	374	374	374	420	404	415	412	429	468	468
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choline monooxygen	2-nitrotoluene dio	choline monooxygen	choline monooxygen	probable dioxygena	probable choline m	probable choline m	probable choline m	w	biphenyl dioxygena	Rieske 2Fe-2S fami	benzoate 1,2-dioxy	probable aromatic-	probable ring hydr	ring hydroxylating	hypothetical prote

ALIGNMENTS

Db 301 FPNNSMLTCSGVEKVWNPIDANTTEVWTYAIVEKDMPEDLKRFLADSVQRTEGPAGFWES 360 OY 361 DDNDNMETASQNGKKYQSRDSDLLSNLGEGEDVYGDAVYPGVVGKSAIGETSYRGEYRAY 420	Db 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 Qy 301 FPNNSMLTCSGVFKVMNPIDANTTEVMTVAIVEKDMPEDKHRFLADSVQRTTGPAGFWES 360	QY 181 ELVGPPGKVVIKANWKAPAENEVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 181 ELVGPPGKVVIKANWKAPAENEVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 Db 181 ELVGPPGKVVIKANWKAPAENEVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 QY 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300	QY 121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	61 IDEVIVSDONDGSIRAFLNVCHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE	QY 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60	Query Match 99.7%; Score 2402; DB 2; Length 449; Best Local Similarity 99.8%; Pred. No. 4.8e-183; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps	A;Gene: ndoB C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;71-119/Domain: Rieske [2Fe-2S] homology <rsk> F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #;</rsk>	A;Accession: JSUU/1 A;Accession: JSUU/1 A;Molecule type: DNA A;Residues: 1-449 <kur> A;Cross-references: GB:M23914; NID:g151392; PIDN:AAB47591.1; PID:g151394 C;Comment: Naphthalene dioxydenase system is composed of three proteins. C;Genetics:</kur>	R;Kurkela, S.; Lehvaeslaiho, H.; Palva, E.T.; Teeri, T.H. Gene 73, 355-362, 1988 A;Title: Cloning, nucleotide sequence and characterization of genes encoding A;Reference number: JS0070; MUID:89211973; PMID:3243438	RESULT 1 JS0071 JS0071 naphthalene dioxygenase (EC 1.14.12) ndoB protein - Pseudomonas putida C;Species: Pseudomonas putida C;Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999 C.Accession. TS0071
						0;	n; Rieske [tein t) #status		ng naphthal	v

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naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfur oxygenase component large ch C;Spectes: Pseudomonas sp.
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
C;Accession: S27632; B49343
R;Denome, S.A.; Young, K.D.
submitted to the EMBL Data Library, February 1992
A;Description: Cloning and molecular characterization of genes involved in metabolis A;Reference number: S27631
A;Accession: S27632
A;Status: preliminary
A;Residues: 1-462 <DEN>
A;Cross-references: EMBL:M60405
A;Cross-references: EMBL:M60405
A;Cross-references: EMBL:M60405
A;Reference number: A49343; MUID:94042852; PMID:8226631
A;Residues: 14-462 <DEN>
A;Cross-references: GB:M60405; NID:9151195; PIDN:AAA16125.1; PID:g294351
A;Cross-references: GB:M60405; NID:g151195; PIDN:AAA16125.1; PID:g294351
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                                                                                                          DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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448; Conser
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99.8%;
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C55217
                                                                                                                  polycyclic aromatic hydrocarbon dioxyge
C;Species: Pseudomonas putida
C;Date: 05-May-1995 #sequence_revision
C;Accession: C55217
A;Title: Identification and characterization of genes encoding A;Reference number: A55217; MUID:94209249; PMID:8157615 A;Accession: C55217 A;Status: preliminary
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C;Superfamily: toluene
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A;Title: Sequences of genes A; Reference number: JN0640; A; Accession: JN0644
                                                                                 R;Takizawa, N.; Kaida, N.; Torigoe, J. Bacteriol. 176, 2444-2449, 1994
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A; Residues: 1-449 <SIM>
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96.7%;
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Pred. No. 2e-178;
0; Mismatches
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PMID:8486285
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C;Superfamily: toluene dioxygenase terminal oxygenase component large chain C;Keywords: 2Fe-2S; heterotetramer; metalloprotein; oxidoreductase; Rieske F;71-119/Domain; Rieske [2Fe-2S] homology <RSX>F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfur oxygenase component large N;Alternate names: nahAc protein C;Species: Pseudomonas putida C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999 C;Date: Trock 1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
                                                                                                                                        FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                    DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                           FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWES
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A; Molecule type: DNA
A; Residues: 1-449 <TAK>
A; Residues: 1-449 <TAK>
A; Cross-references: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
A; Cross-references: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [2F C; Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F; 71-119/Domain: Rieske [2Fe-2S] homology <RSK>
F; 81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status pi

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A/Gene: ntdAc C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Ri C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Ri C;Seywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;69-117/Domain: Rieske [2Fe-2S] homology <RSK>F;79,81,99,102/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #s1
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-447 < PAR>
A; Cross-references: GB:U49504; NID:g1773273;
A; Experimental source: strain JS42
C; Comment: This enzyme catalyzes the addition
C; Genetics:
                                                                                                                                                                                                                                                  Gene 181, 57-61, 1996
A;Title: Cloning and sequencing of the genes encoding 2-nitrotoluene A;Reference number: JC5350; MUID:97128768; PMID:8973308
A;Accession: JC5352
                                                                                                                                                                                                                                                                                                                            2-nitrotoluene dioxygenase (EC 1.14.12.-) iron-sulfur protein large chain - RALTERIAN CARRELLE PROTEIN ALPHA CHAIN C.; Species: Pseudomoas sp.
C.; Date: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Aug-1999 C; Accession: JC5352
RE; Parales, J.V.; Kumar, A.; Parales, R.E.; Gibson, D.T.
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JC5352
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83.7%;
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94.4%; Pred. No. 3.8e-174;
tive 13; Mismatches 12;
   34;
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Score 2051; DB 2;
Pred. No. 3.8e-155;
4; Mismatches 37;
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               QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                     DDNENMETLSQNAKKYQSSNSDQIASLGFGKDVYGDECYPGVVGKSAIGETSYRGFYRAY
                                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                    FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES
                                                                                                                                                             QMTSKYGSGMGLTWDYYSGNFSADMVPDLMAFGAAKQEKLAKEIGDVRARIYRSILNGTV
                                                                                                                                                                                      QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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QAHISSSNWAEFENASRNWHTELTKTTDR
                                                                                                         FPNNSFLTGSATFKVWNPIDENTTEVWTYAFVEKDMPEDLKRRLADAAQRSIGPAGFWES
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A; Molecule type: DNA
A; Residues: 1-459 <ROI
A; Cross-references: EY
C; Genetics: A;Genome: plasmid pNL1 c;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R:C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R:C;Keywords: 2Fe-25; metalloprotein; oxidoreductase; Rieske iron-sulfur protein E;80,82,100,103/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #s naphthalene dioxygenase (EC 1.14.12.-) large chain - C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #t C;Accession: T31134
C;Accession: T31114
C;Accession: T31114
C;Accession: T31124
C;Accession: T31124
C;Accession: T31134
A; Gene: bphAlf A; Status: preliminary; A; Reference number: A; Accession: T31134 Query Match Best Local Matches Similarity Conservative <ROM> EMBL:AF079317; NID:g3378261; PID:g3378275; PIDN:AAD03858 lete sequence Z20992 translated 39.6%; 71; Score 955; DB 2; Pred. No. 5.4e-68; 1; Mismatches 162 from GB/EMBL/DDBJ catabolic Thurston, 162; #text_change 19-May-2000 Length 459 Sphingomonas aromaticivorans plasmid Indels S.J.; Sisk, from 12; E.C.; Sphingomonas Gaps Rieske 7; #status G Σ

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GKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAA-LPPEGAGLQMTSK

LDKSKLGLAPI-RVETYKGFIFGCHDPEAPSLEDYLGDFCWYLDTIWDGPDGGLELLGPP

185

LNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK-HSGGLELVGPP 186

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67

RQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGES

RQPDGSLKAFINSCTHRGNQICHADSGSAKAFVCNYHGWVFGQDGSLVDVPMEERCYHSD

8 8

YRAYQAHVSSSNWAE

431

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terminal oxygenase component large chain homolog - Sphingomonas aromaticivo C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000 C;Accession: T31256 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston. S.T. Sieb F.C. R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston.
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C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
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A; Accession: T31256
A; Status: preliminary; translated
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A; Residues: 1-450 < ROM>
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                                                                                             NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAG
                                                                                                                                                                           AGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHL
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LFDNDDGDNLTACTEQSRGWRTAQMDVYTNMALGRSGKREG-FPGDIAAGLVSEHNQRYF
                                   FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGF
                                                                         NITIFPNLQLLPGLNWFRVYHPKGPGQIEQWTWAMAENDMPEAVKAQILENQCLTFGLAG
                                                                                                                                                   -GLSVAGMNGHMVLSALDGVSGYAFYPDPKPILEYLEANRQTVIDRLGEVRGRQVWGAQV
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RESULT 8
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biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain C:Species: Escherichia coli
C:Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: A65031; S49292
C:Accession: A65031; S49292
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A;Roslecule type: DNA
A;Residues: 1-19; A', 21-383, 'ATAPATANCVWKW', 397-398, 451, 'R', 453, 'SAATTAFLALLTISFQKLPL
A;Cross-references: EMBL:Z37966; NID:g550595; PIDN:CAA86018.1; PID:g550596
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
E;75-123/Domain: Rieske [2Fe-2S] homology <RSK>
F;85,87,105,108/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
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R;Turlin, E.; Gasser, F.; Biville, F.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and sequencing of an E. coli gene
A;Reference number: S49292
A;Accession: S49292
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R:Blattner, F.R.; Plunkett III,
A: Rose, D.J.; Mau, B.; Shao,
Science 277, 1453-1462, 1997
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                                        YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                 GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA
                                                                                                                            GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
                                                                                                                                                                          AGHNN - - IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
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                                                                                                                                                                                                                                                                                                                                                                                               AENFVGDAYHVGWTHASSL-----
                                                                                                                                                                                                                                                                                                         --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
                                                                                                                                                                                                                                                                                                                                                    AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD-----GQTARPVWETAKDALQFG
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Mau, B.; Shao, Y.
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shina DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia co A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Recession: D91054
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-453 < HAY>
A; Residues: 1-453 < HAY>
A; Cross -references: GB:BA000007; PIDN:BAB36827.1; PID:g13362875; GSPIA; Experimental source: strain 0157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: EC34044
C; Superfamily: toluene dioxygenase terminal oxygenase component large C; Keywords: oxidoreductase
A;Title: Genome sequence of e
A;Reference number: A85480; M
A;Accession: G85898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-453 <STO>
                                                                                                                                                                                  biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: G85898
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blphenyl dioxygenase (EC 1.14...) terminal oxygenase component large chain C; Species: Escherichia coli
C; Pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2001 C; Pate: D91054
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, F.; Hattori, M.; Shinaqawa, H.;
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Yasunaga, T.; Kuhara, S.;
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80; MUID:21074935; PMID:11206551
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Pred. No. 1.6e-50;
4; Mismatches 174
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Shiba, T.; Hattori, M.; !
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M.; Shinagawa,
                                                                                                                                                        O157:H7
                                                                                                                                                                                                                  J.D.; Rose, Potamousis,
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DYSRYMDLKEGWLDRR--IFSDADIYEEELYRIFARSWLFVAHESQIPSSGDFLTTHMGE

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C; Key
F; 88,
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                                                                                                                                         A; Note: bphAlb C; Superfamily:
                                                                                                                                                                              A; Genome:
                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-455 < ROM>
                                                                                                                                                                                                                                                                                    A; Accession: T31258
                                                                                                                                                                                                                                                                                                     R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas A;Reference number: Z20992
                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                           aromatic oxygenase large chain - Sphingomonas aromaticivorans plasmid C; Species: Sphingomonas aromaticivorans
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                                                                                                  Superfamily: toluene dioxygenase terminal oxygenase component large chain; Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein; Reywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein; 88,90,108,111/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                    Query Match
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                                   83;
                                            Score 723.5; DB 2
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                                   169;
                                                                                                                                                                                                              PID:g3378399;
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benzene 1,2-dioxygenase (EC 1.14.12.3) terminal oxygenase component large chain - Pseudo C; Species: Pseudomonas putida C; Date: 19-May-1994 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000 C; Accession: JN0812 R; Tan, H.M.; Tang, H.Y.; Joannou, C.L.; Abdel-Wahab, N.H.; Mason, J.R. Gene 130, 33-39, 1993
A; Title: The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenase are un A; Reference number: JN0810; MUID:93345820; PMID:8344526
A; Residues: 1.450 <TAN>
A; Residues: 1-450 <TAN>
A; Residues: 1-450 <TAN>
A; Residues: 1-450 <TAN>
A; Experimental source: strain ML2
C; Comment: This enzyme is involved in catalyzing the oxidation of benzene to cis-1,2-dil-C; Comment: The reduced enzyme catalyzes the oxidation of benzene to cis-benzene dihydrod A; Genetics:
A; Gene: bedC1
A; Genome: plasmid
C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [2Fe C; Reyvords: ZFe-25; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; Rie F; 96, 98, 116, 119/Binding site: ZFe-25 cluster (Cys, His, Cys, His) (covalent) #status pre
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WKAPAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
                                                                                      --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                                     VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE---
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                                                       PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
                                                                                                                                 QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFIGGCIKSVISANWKFGVENFIGDAYHAGWTHDSGTR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYDAGDIDFKNHGLKNVAKVGNYKGLVFATFNSDAPSLEAWLGDFRWYLDMILDNEEGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAVIVARQPDGSIRVMLNSCPHRGNKVCFADAGNTRRFVCNYHGWAFDTAGDLKGMHEEY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEK 121
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                    27.0%;
                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                        Score 650.5;
                                                                                                                                                                                                                                                                                       ed. No. 8.4e-44;
Mismatches 174;
                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                        Length
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                 EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP
                                                     TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS
                                                                                                                                                                   GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
                                                                                                                                                                                                      VLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                                               WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                                                                                                                                                                                                                                                                                                    --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                    VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
                                                                                          PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
                                                                                                                           TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWESDDNDNME
                                                                                                                                                                                                                                                                                 WKAPAENFYGDAYHYGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                                                                                                                                                 QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLN
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194

148

94 79

208

251

383

367 321

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A;Gene: todCl
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidorec
F;86-134/Domain: Rieske [2Fe-2S] homology <RSK>
F;96,98,116,119/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                                                                                                                                                                                                                                                                          R;Zylstra, G.J.; Gibson, D.T.
J. Biol. Chem. 264, 14940-14946, 1989
A;Title: Toluene degradation by Pseudomonas
A;Reference number: A36516; MUID:89359301; F
A;Accession: A36516
                                                                                                                                                                                                        A; Cross-references: GB:J04996; A; Experimental source: strain I C; Genetics:
                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-450 <ZYL>
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pseudomonas putida
C;Date: 15-Feb-1991 #sequence_revision
C;Accession: A36516
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                                         Query Match
Best Local
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Mac
Local 5,
145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
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                                       Similarity
                     Conservative
                                     26.9%;
                                                                                                                                                                                                                              ; NID:g151600;
F1
                 71;
                 Score 648.5; DB 1;
Pred. No. 1.2e-43;
1; Mismatches 181;
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                                                                                                                                                                                                                                                                                                                                  ; putida F1.
PMID:2670929
                                                                                                                                                                                                                                                   PIDN: AAA26005.1;
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                   Indels
                                                          Length
                                                                                                                                                                                                                                                                                                                                                          Nucleotide
                                                                                                                                                                                                                                                 PID:g15160:
                                                            450;
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                 25;
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               Gaps
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oxidoreductase;
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RESULT 15
BA1858
blphenyl dioxygenase (EC 1.14.12.-) terminal oxygenase component large chair C. Species: Pseudomonas sp. C. Species: Pseudomonas sp. C. Date: 04-Mar-1993 #sequence_revision 06-Jan-1995 #text_change 05-May-2000 C. Accession: B41858
R. Erickson, B.D.; Mondello, F.J. J. Bacteriol. 174, 2903-2912, 1992
A. Title: Nucleotide sequencing and transcriptional mapping of the genes enco
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A; Residues: 1-461 <AST>
A; Cross-references: EMBL: X80041;
A; Cross-references: Expain P6
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S51757
R;Asturias, J.A.; Diaz, E.; Timmis, K.N.
submitted to the EMBL Data Library, July 1994
A;Description: Evolutionary relationship of the biphenyl dioxygenase of the A;Reference number: S51757
A;Accession: S51757
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGMGVLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVRARIYRSHLNCTVFPNNS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALP------PEGAGLQMTSKYG 247
                                                                                                                                                                                                                                                                                                                                       WVEIQSVLRGHKARSRPFNAEMSLRETNTADPDWPGTI-SYVYSEEAARGFYAHWSRMMT
                                                                                                                                                                                                                                                                                                                                                                           METASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVS 425
                                                                                                                                                                                                                                                                                                                                                                                                                      FLPGINTIRTWHPRGPHEIEVWSFTVVDADAPAEIKEEYRRQTIRTFSAGGVFDQDDGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWESDDNDN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAEQFCSDMYHVGTTSHLSGLLAG------LPDEIDIREVQPPTTGIQYSAPWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D₩
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYTDEALYQQELELIFGRSWLLLGHETQIPKAGDFMTQYMGEDPVIVSRQRDGSISVFLN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 637; DB 2;
Pred. No. 1e-42;
4; Mismatches 187
      transcriptional mapping of the genes encoding bipheny
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A;Gene: bphA1; bphA
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske
C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase;
F;90-138/Domain: Rieske [2Fe-2S] homology <RSK>
F;100,102,120,123/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #stat
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A; Residues: 1-459 <ERI>
A; Cross-references: GB: M86348; NID: g349602;
A; Experimental source: strain LB400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIN:97256, NCBIP:97259) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A41858; A; Accession: B41858
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Best Local
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VYAEEAARGMYHHWMRMMSEPSWA
                                           AIGETSYRGFYRAYQAHVSSSNWA 430
                                                                                                                                                                                    VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR 372
                                                                                                                                                                                                                                                                             QIPTK-GNQFRAAWGGHGSGWYVDEPGSLLAVMGPKVTQYWTEGPAAELAEQRLGHTGMP
                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKGLLDPR-IYADQSLYELELERVFGRSWLLLGHESHVPETGDFLATYMGEDPVVMVRQK 89
                                                                                           HNIRNFSAGGVFEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y 431
                                                                                                                                      SVQRTTGPAGFWESDDNDNMETASQNGKKYQSRDSDLLLSNLGFGEDVYGDAVYPGVVGKS 406
                                                                                                                                                                                                                               VRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                                                                                                                                           GGMQKWVIPCNWKFAAEQFCSDMYHAGTTTHLSGILAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKSIKVFLNQCRHRGMRICRSDAGNAKAFTCSYHGWAYDIAGKLVNVPFEKEAFCDKKEG 149
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146; Conserv
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Pred. No. 5.3e-41;
9; Mismatches 186
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Maximum Match 100%
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2051.298 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution to have a being printed,

SUMMARIES

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449	449	449	449	449	449	449	449	449	449	Length DB
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AAB12583	AAB12578	AAB12577	AAB12582	AAB12581	AAB12579	AAB12567	AAB12566	AAB12565	AAB12580	ID
Naphthalene dioxyg			Naphthalene dioxyg	Naphthalene dioxyq	Naphthalene dioxyq	NDO related comple	NDO related comple	Naphthalene dioxyg	Naphthalene dioxyg	Description

Novel naphthalene dioxygenase mutant having a specific amino acid

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העדממפט מווידווס מכינת	tt ttabur	motif in D	motif in	+	Novel human diagno	Herbicidally activ	Human oxygenase-li	Spinach choline mo	Sugarbeet choline	triplex hortens	album choline	album choline	C album choline mo	Pseudomonas aerugi	Corynebacterium gl	C glutamicum prote	Klebsiella pneumon	Benzene dioxygenas	РСВ	PCB deco	c dih	Benzene ring hydro	rrabacter oxida	ular	a sp.	related compl	related	related	related	related	related compl	related	related	hthalene diox	NDO related comple	

ALIGNMENTS

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RESULT 1
AAB12580
ΧX
                 WPI; 2000-452174/39.
N-PSDB; AAA65354.
                                                                                                                                                                                                  Pseudomonas sp. strain NCIB(9816-4) naphthalene dioxygenase; NDO; inducible multi-component enzyme;—a1pha subunit; mutant; chiral diol; polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                             09-NOV-2000 (first entry)
                                                Parales R,
                                                                                                           26-OCT-1999;
                                                                                                                                                                                                                                           Naphthalene dioxygenase mutant F352T protein sequence SEQ ID
                                                                                                                                                                                                                                                                                   AAB12580;
                                                                                                                                                                                                                                                                                                     AAB12580 standard; Protein; 449 AA
                                                                   (IOWA ) UNIV IOWA RES FOUND
                                                                                       26-OCT-1998;
                                                                                                                               29-JUN-2000.
                                                                                                                                                   WO200037480-Al
                                                                                                                                                                       Synthetic.
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                                               Gibson D,
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                                               Resnick S,
                                                Lee
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RESULT 2
AAB12565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C(-)-(15,7R)-(15-napththalene dhlydrodiol, (-or +)-(15-bhplenyl-)-4-
Cdihydrodiol, (15,7R)-cis-hphenanthrene-1,2-dihydrodiol, cis-1,2-
Cdihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
Cdihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
Challene, and 1,2-dihydronaphthalene respectively. The polypeptides and
Cthe host cells are also useful for preparing 1,2-dihydroxy-1,2-
Cdihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which
Chost cells are also used in bioremediation in which they oxidise an
Caromatic compound such as indene, 1,2-dihydronaphthalene,
Chost cells are also used in bioremediation in which they oxidise an
Caromatic compound such as indene, 1,2-dihydronaphthalene,
Caenaphthylene, naphthalene, 1,0-dihydroanathrene, dibenzo(1,4)dioxan,
Caenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan,
Caenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan,
Caenaphthylene, dihydro dihydroxy compound. The polypeptides and the host
Cells are useful for preparing chiral diols for use in the polymer,
Cresin, pharmaceutical or rubber industry. The present sequence represents
Caromatic compound second in the present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related complex (I) comprising several polypeptides which contain a alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
AAB12565
                                      AAB12565 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                        421
                                                                                                                                    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a naphthalene dioxygenase (NDO) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                      QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                                                                                                                                                                                                                                                                                                       QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                             FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                  QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                              DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                           FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                     QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                ELYGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                    Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2409; DB 21;
Pred. No. 4.5e-225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                      AA
                                                                                                                                                                        449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NDO) or NDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Q

Вb

121 61 61

KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL

IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120

120

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Вр
                               Q
                                                                      Matches 448;
                                                                                                        Query Match
                                                                                                                                                                         aromatic compound such as indene, 1.2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1.4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzoturan, dibenzoturan, yl0-dihydroanthracene, or 9,10-dihydroanthracene, or 9,10-dihydrophenanthracene corresponding dihydro dihydroxy compound. The polypeptides and the hosells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                      related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (-or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also used in bioremediation in which they oxidise an involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an host cells are also used in bioremediation in which they oxidise and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDC inducible multi-component enzyme; alpha subunit; mutant; chiral polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a naphthalene dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parales R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2000 (first entry)
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas sp
                                                                                         Local
                  1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-452174/39.
 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Page 58-60; 151pp; English
                                                                                       Similarity
                                                                                                                                            449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dioxygenase
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US25079
                                                                                       99.8%;
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                                                                      0;
                                                                                       Score 2404; DB 21; Pred. No. 1.4e-224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F352V protein
                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                          21;
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                                                                                                      Length 449;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NDO) or
                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDO;
                                                                                                                                                                                                  represents the
                                                                      Gaps
                                   60
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RESULT 3
AAB12566
ID AAB1
XX AAB1
XX AAB1
XX Pseu
KW Pseu
KW Indu
KW Pseu
KW Indu
KW Poly
XX Pseu
OS Synt
XX 29-J
XX 29-J
XX 26-C
XX 26-C
XX 26-C
XX 26-C
XX 26-C
XX 26-C
XX 27-C
PF 26-C
XX 27-C
PF 26-C
XX 2
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                          The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxy-1,2,3,4-tertahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral diol; polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IOWA ) UNIV IOWA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                               Pseudomonas
                                                                                                                                         Pseudomonas sp. strain NCIB 9816-4; naphthalene inducible multi-component enzyme; alpha subunit;
                                                                                                                                                                                                                 09-NOV-2000
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26-OCT-1999;
                            29-JUN-2000
                                                        WO200037480-A1
                                                                                                                                                                                  NDO related complex alpha subunit protein sequence
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QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                               FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
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Pred. No. 1.4e-224;
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Matches 448; Query Match Best Local

Similarity

99.8**%**;

Score 2404; DB 21; Pred. No. 1.4e-224;

DB 21;

Length Indels

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Gaps

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Conservative

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RESULT 5
AAB12579
The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (I) comprising several polypeptides which contain an C alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-C dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cis-locate involves contacting them with naphthalene, biphenyl, phenanthrene, C indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-C dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which cells are also used in bioremediation in which they oxidise an C involves contacting them with phenanthrene. The polypeptides and the compatitic compound such as indene, 1,2-dihydronaphthalene, cells are also used in bioremediation in which they oxidise an C aromatic compound such as indene, 1,2-dihydronaphthalene, cells are useful for preparing thenyl, fluorene, dibenzo(1,4)dioxan, cenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, cenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, cenaphthylene, paphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer. C anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the cexamplification of the present invention.
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substitution for preparing chiral diols for use in the polymer, r.
pharmaceutical or rubber industry and for carrying out bioremedia
Sequence
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                                           Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
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         Page 131-133; 151pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 448;
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                                                       Naphthalene dioxygenase mutant F352I protein sequence SEQ ID
                                                                                                                     09-NOV-2000
                                                                                                                                                                                                                                        AAB12582 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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Pred. No. 1.7e-224;
0; Mismatches 1;
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Pseudomonas sp.

strain NCIB 9816-4; naphthalene dioxygenase;

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involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1.2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1.2-dihydroxy-1.2-cdihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1.2-dihydronaphthalene, oxidise an aromatic compound such as indene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, acenaphthylene, paptidioxan, biphenyl, fluorene, oxidise and the host cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia
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N-PSDB; AAA65356.
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polymer; resin; pharmaceutical; rubber industry; bioremediation.
181
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                                                    ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2403; DB 21;
Pred. No. 1.7e-224;
0; Mismatches 1;
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bioremediation
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The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-cdihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
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                                                                                                                                      WO200037480-A1
                                                                                                                                                               Synthetic
                                                                                                                                                                                                     polymer;
                                                                                                                                                                                                              Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d
                                                                                                                                                                                                                                                                                09-NOV-2000
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CC involves contacting them with naphthalene, biphenyl, phenanthrene, clindene, and 1.2-dihydronaphthalene respectively. The polypeptides and cthe host cells are also useful for preparing 1.2-dihydroxy-1.2-cc dihydrophenanthrene or 3.4-dihydroxy-3.4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the clindentic compound such as indene, 1.2-dihydronaphthalene, or aromatic compound such as indene, 1.2-dihydronaphthalene, cc benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, cc dibenzothiophene, 9.10-dihydroanthracene, dibenzofuran, cc dibenzothiophene, 9.10-dihydroanthracene, or 9.10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cc clls are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cc exemplification of the present invention.
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                                                                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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RESULT

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                                                                                                                                                                                           CC The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (1) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)-(15.2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3.4-CC dihydroxyindan, 1.2-dihydroxy-1, 2.3.4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1.2-dihydroxy-1, 2.3.4-tetrahydronaphthalene, which CC involves contacting them with naphthalene respectively. The polypeptides and the host cells are also useful for preparing 1.2-dihydroxy-1, 2-CC dihydrophenanthrene or 3.4-dihydroxy-3.4-dihydrophenanthrene which CC involves contacting them with phenanthrene. The polypeptides and the host cells are also useful for benanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1.2-dihydronaphthalene, CC acenaphthylene, naphthalene, anthracene, phenanthrene, dibenzo(1.4)dioxan, CC dibenzothiophene, 9.10-dihydroanthracene, or 9.10-dihydrophenanthrene a CC corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, CC exist, pharmaceutical or rubber industry. The present sequence represents an apphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC exemplification of the present invention.
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                                                                                                          Query Match
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Matches 448
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                                                                                                                                                                         Sequence
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                                            IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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                                                                                                           Mismatches
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                                                                                                                      DB 21;
2.2e-224;
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The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,

Claim 13;

Page 102-103; 151pp;

English.

or NDO

dihydroxyindan,

1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
                                                                                                                                                                                            Parales
                                                                                                                                                                                                                                                         26-OCT-1999;
                                                                                                                                                                                                                                                                                                 WO200037480-A1
                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
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                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                     polymer;
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DB; AAA65342.
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                                                                                                                                                                                                                                                                                                                                                                        strain NCIB 9816-4; naphthalene dioxygenase; NDO;
                                                                                                                                                                                                                                                                                                                                                     pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 447
                                                                 Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral colliner; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                      AAB12584 standard;
                                                                                                                                 Naphthalene
                                                                                                                                                              09-NOV-2000
WO200037480-A1
                                         Pseudomonas
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                                                                                                                                                                                                                                                                                                             QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                         DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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Pred. No. 4.2e-224;
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FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES

360

300 300 240 240 180

360

FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTYGPAGFWES

KDLYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL

180

0

QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV

QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (1) comprising several polypeptides which contain an alpha subunit that contains substituted and several subunit that contains substituted and several positions. The polypeptides and host cells are useful for preparing (-)-(1S,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dihydroxyIndan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, Indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Pred. No. 6.6e-224;
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Similarity

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                            The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (I) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing (-1-(15,78)-cis-naphthalene dihydrodiol, (-0+)-cis-biphenyl-3,4-CC dihydroxyindan, 1,2-dihydroxy-1,2-3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, clindene, and 1,2-dihydroxy-1,2-3,4-tetrahydroxphaphthalene, which involves contacting them with naphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-CC dihydroxphenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the clinder compound such as indene, 1,2-dihydronaphthalene, or aromatic compound such as indene, 1,2-dihydronaphthalene, cells are also used in bioremediation in which they oxidise an accompathylene, naphthalene, anthracene, phenanthrene, dibenzo(1,4)dioxan, cells are useful for preparing them phenanthrene, dibenzo(1,4)dioxan, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer.
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N-PSDB; AAA65343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia.
                                                    WPI; 2000-452174/39
N-PSDB; AAA65344.
                                                                                                                       (IOWA ) UNIV IOWA RES
                                                                                                                                                                                                                                                                                              Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral conformer; resin; pharmaceutical; rubber industry; bioremediation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
  09-NOV-2000
                                        AAB12571;
                                                                              AAB12571 standard; Protein; 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related complex (I) comprising several polypeptides which contain a alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13;
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                                                                                                                                                                                     QAHVSSSNWAEFEDASSTWHTELTKTTDR
                                                                                                                                                                                                                                                               DUNDNMETASQNGKKYQSRDSDLLSNLGFGKDYYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                      FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                         QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                          DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                               QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGSKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFASLAGNAVLPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPIFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434;
                                                                                                                                                                                                                                                                                                                                                FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 105-107; 151pp; English.
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(first entry)
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96.78;
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Pred. No. 6e-219;
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Best Local S
Matches 429
                                                                                                                                                                                                                                                                                                                                                                   aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzofuran, 2,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with nephthalene, bibhenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-the polypeptides and dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related complex (I) comprising several polypeptides which contain an alpha subunit that contains substitution acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 107-109; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA65345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a naphthalene dioxygenase (NDO) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND
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IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                   MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIXARNWLFLTHDSLIPSPGDYVTAKMG
                                                                                                                                            MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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429; Conserv
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                                                                                                                                                                                                                                                                                                                449 AA;
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                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                 Score 2318; DB 21;
Pred. No. 3.1e-216;
2; Mismatches 8;
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                                                                                                                                                                                                                                                             449;
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IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120

	O-	421	В
	QAHVSSSNWAEFEHASSTWHTELTKTTDR 449	421	Ş
420	DDNDNMETASQNGKKYQSRDSDLISNLGFGKDYYGDAYYPGVVGKSAIGETSYRGFYRAY 420	361	Ф
420	DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY	361	γO
360	FPNNSVLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADAVQRTVGPAGFWES	301	В
360	0.	301	δÃ
300	QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVPARIYRSHLNCTV	241	Вb
300	-	241	δŌ
240	ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRTGESIFSSLAGNAVLPPEGAGL	181	ф
240	-	181	Qγ
180	KELYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPSLMDYLGDAAWYLEPTFKHSGGL	121	В
180	_	121	VΩ

Search completed: January 27, 2003, 08:58:50 Job time: 31.1667 secs

rapb

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
       Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/U2

2: /cgn2_6/ptodata/1/pubpaa/U3

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Gapop 10.0 , Gapext 0.5
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//cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
μ,	737	30.6	453	10	US-09-815-242-10253	Sequence 10253, A
2	377	15.7	490	9	US-09-738-626-6140	
w	376.5	15.6	385	10	US-09-815-242-11692	Sequence 11692, A
4	339.5	14.1	424	10	US-09-815-242-5097	
ر ت	185	7.7	35	10	US-09-776-490-19	
o	185	7.7	35	10	US-09-776-491-19	19,
7	174	7.2	35	10	us-09-776-490-20	20,
8	174	7.2	35	10	١.	20,
9	168	7.0	35	10	US-09-776-490-21	
10	168	7.0	35	10	US-09-776-491-21	Sequence 21, Appl
11	118.5	4.9	354	ר	US-08-976-063C-4	Sequence 4, Appli
12	110	4.6	35	10	US-09-776-490-12	Sequence 12, Appl
13	110	4.6	35	10	US-09-776-491-12	Sequence 12, Appl
14	109	4.5	35	10	US-09-776-490-14	Sequence 14, Appl
15	109	4.5	35	10	US-09-776-491-14	Sequence 14, Appl
16	108	4.5	35 5	10	US-09-776-490-13	Sequence 13, Appl
17	108	4.5	3 5	10	US-09-776-490-15	Sequence 15, Appl
18	108	4.5	35	10	US-09-776-491-13	13,
19	108	4.5	35	10	US-09-776-491-15	Sequence 15, Appl

Query Match
Best Local Similarity

30.6%;

Score 737; DB 10; Pred. No. 1.6e-57;

Length 453;

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
93	94	94	94.5	95	95	100	100	101	101	101	101	101	101.5	102	102	102	102	103	103	104	104	106	106	107.5	107.5
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US-09-776-490-16	US-09-815-242-12265	US-09-815-242-5654	US-09-925-301-1362	US-09-776-491-46	US-09-776-490-46	US-09-776-491-17	US-09-776-490-17	US-09-712-363-246	US-09-776-491-45	US-09-776-491-44	US-09-776-490-45	US-09-776-490-44	US-09-738-626-6115	US-09-776-491-10	US-09-776-491-8	US-09-776-490-10	US-09-776-490-8	US-09-776-491-11	US-09-776-490-11	US-09-776-491-18	US-09-776-490-18	US-09-776-491-9	US-09-776-490-9	US-09-924-097-15	US-10-047-542-78
Sequence 16, Appl		Sequence 5654, Ap	Sequence 1362, Ap	Sequence 46, Appl	`	Sequence 17, Appl	`	Sequence 246, App	`	Sequence 44, Appl	•	Sequence 44, Appl	Sequence 6115, Ap	Sequence 10, Appl	8, 2	_	Sequence 8, Appli			Sequence 18, Appl	18,		Sequence 9, Appli		Sequence 78, Appl

ALIGNMENTS

PRIOR FILING DATE: 2001 NUMBER OF SEQ ID NOS: 1 SOFTWARE: FastSEQ for W SEQ ID NO 10253 LENGTH: 453 TYPE: PRT ORGANISM: Escherichia US-09-815-242-10253	FILING DATE: APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION N APPLICATION N	Xu, H. NVENTION: NVENTION: NVENTION: NVENTION: ENCE: ELIT ENCE: ELIT PLICATION LING DATE: ICATION NU LING DATE: ICATION NU LICATION NU	RESULT 1 US-09-815-242-10253 Sequence 10253, Application U Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith APPLICANT: Wall, Daniel APPLICANT: Wall, Daniel APPLICANT: Carr, Grant J. APPLICANT: Carr, Grant J. APPLICANT: Carr, Grant J. APPLICANT: Carr, Grant J.
2001-02-16 DS: 14110 For Windows Version 4.0 Phia coli		Howard Howard I Identification of Essential Genes in I Prokaryotes LTRA.011A N NUMBER: US/09/815,242 PE: 2001-03-21 NUMBER: 60/191,078 1 2000-03-21 NUMBER: 60/206,848 1 2000-05-23 NUMBER: 60/207,727	lication US/09815242 51569A1 ck, Robert ckari L. di, Judith W. Daniel ck, John D. crant J. drant J. dr

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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6140
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                                                                                                                                                                                   PRIOR FILING DATE: 2000-08
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.1
SEQ ID NO 6140
                                      Matches 118;
                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6140, Application US/09738626 Publication No. US20020197605A1
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                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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                                                                                                                                                                      LENGTH: 490
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IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----AEQRLGEVRALRL 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD-----GQTARPVWETAKDALQFG
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IKEDA, MASATO
OZAKI, AKIO
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OCHIAI, KEIKO
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                                      Conservative
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                                    Score 377; DB 9;
Pred. No. 1.4e-25;
6; Mismatches 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 174;
                                                                        Length 490;
                                      Indels
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                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 11692
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Query Match
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PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                 PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                      PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
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                                                      ORGANISM: Klebsiella
                                                                         TYPE: PRT
                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                          APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick, John D. Carr, Grant J.
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Zyskind, Judith W.
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Score 376.5;
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Length 385;
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; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5097
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                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5097
LENGTH: 424
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                                                Matches
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                                                                                                                                                                                TYPE: PRT
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  25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
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APPLICATION NUMBER: 60/242,578
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                                                Conservative
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27.3%;
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                                           Score 339.5; DB 10;
Pred. No. 2.4e-22;
1; Mismatches 177;
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8; Mismatches 154;
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                                                                                       DB 10;
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                                                                                                                                INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 EILESCQ---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 DNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
MOLECULE TYPE: protein
                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS-----ADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPN--- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAKVCAERQGNSQRFTCPYHGWTYDSHGSLIGLP-DKAAYQHA--GQCHPELSLTQVKHA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGV-DAYHLPFAHKRYLEYLNTL------GTDPESHKRHGRG-EALGNGHALI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKC---LGLKEVARV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDILGLN--IRSFFPTAADEVSVTVWGAGFADETREERAARINGLISFIGPGGFGTPDDV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VYRNFLFIHYGARQASLETYLGQAKDYIDLICDQSEAELEIIPGGFEHSIKANWKLLAE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISGPPSTGRPIAYWSPLFPEALKPSIAAKFERLVERFGQARAEDIAHTNKSLFIFPNLVI 304
                                                                                                                                                                                                                                        NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Charlotte STATE: No. US20010012886A1th Carolina
                                       STRANDEDNESS: <Unknown>
                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Drawer 34009
                                                                                  LENGTH: 35 amino acids
                                                                                                                                                       TELEX: 575102
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RESULT 7
US-09-776-490-20
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US-09-776-491-19
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Patent No. US20010013135A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
     Sequence 20, Application US/09776490 Patent No. US20010012886A1
                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                               1 NVCRHRGKTLVSVEAGNAKGPVCSYHGWGFGSNGK 35
                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: BELL, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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STATE: No. US20010013135Alth Carolina
                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 35 amino acids
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Drawer 34009
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Pred. No. 3.2e-10;
                                                                                                                                                                                                    Score 185; DB 10;
Pred. No. 3.2e-10;
                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                           DB 10;
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                                                                                                                                                                                                                       Length 35;
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; Sequence 20, Application US/09776491
; Patent No. US20010013135A1
; GENERAL INFORMATION:
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APPLICANT: Briggs, Steven P
Johal, Gurmukh S
Grav, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                        79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
|||||||||||: |||||| || |||||:
1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
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APPLICATION NUMBER: US 08/810,009

EILING DATE: 04-MAR-1997

ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                         APPLICANT: Briggs, Steven
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CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                        CITY: Charlotte
                                                                         STATE: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. Dr
CITY: Charlotte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                               Johal, John
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P.O. Drawer 34009
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                                                                           US20010013135A1th Carolina
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                                                                                                                                                                                                                                        , Steven P. Gurmukh S.
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                                                                                                                                                                  CELL DEATH AND DISEASE RESISTANCE IN PLANTS: 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 174; DB 10;
Pred. No. 3.1e-09;
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RESULT 9
US-09-776-490-21
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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APPLICATION NUMBER: US 08/810,009
EILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                            APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         CITY: Charlotte
STATE: No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/810,009
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85.7%;
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Pred. No. 3.1e-09;
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RESULT 10
US-09-776-491-21
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Best Local Similarity
Matches 28; Conserv
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                   Query Match
Best Local :
 Matches
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INFORMATION FOR SEQ ID NO: 21:
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Local Similarity 80.0
nes 28; Conservative
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                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray, John TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
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ADDRESSEE: BELL, SELTZER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Charlotte STATE: No. US20010013135A1th Carolina
                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                LENGTH: 35 amino acids
                                                                                                                                                                                                                                                       TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
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                 80.0%;
               7.0%; Score 168; DB 10.0%; Pred. No. 1e-08;
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Pred. No. 1e-08;
Mismatches
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                                  DB 10; Length 35;
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Indels
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Best Local Similarity
Watches 56; Conserva
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US-08-976-063C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: BATELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 196
FILING DATE: 29-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: HP VECTRA
OPERATING SYSTEM: DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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   208
                                    240
                                                                  149 DNLM-DLTHETYVHASSIGQKEIDEAPVSTRVEGDTVITSRYMDNVMAPPFWRAALRGNG 207
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CITY: Tarrytown
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kurt G. Briscoe
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                          1 MFPKNAWYVACTPDEIADKP---LGRQICNEKIVFYRGPEGRVAAVEDFCPHRGAPL---
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                                   L 240
                                                                                                     ENFVGDAYHVGWTHASSLR---
                                                                                                                                     ERYGFIWVWPGDRELADPALIHHL---EWADNPEWAYGGGL-----YHIACDYRLMI 148
                                                                                                                                                                     SFHGFIY---GCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPA 199
                                                                                                                                                                                                        ----SLGFVRDGKLICGYHGLEMGCEGKTLAMP------GQRVQGFPCIKSYA-VE 99
                                                                                                                                                                                                                                       EAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLG----LKEVARVE 142
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   208
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alexander Steinbuchel; Horst Priefert; Jurgen I
VENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION (
VENTION: CONIFERYL ALCOHOL, CONIFERYLALDEHYDE,
VENTION: ACID AND THEIR USE
                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                          4.9%; Score 118.5; DB 1; 23.2%; Pred. No. 0.007; ative 40; Mismatches 78;
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                                                                                                     SGESIFSS-LAGNAALPP----EGAG 239
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US-09-776-491-12
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US-09-776-490-12
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ADDRESSEE: BELL, SELTZER, STREET: P.O. Drawer 34009
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TELEX: 575102
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Sequence 12, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
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Patent Mo. US20010012886A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                       79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
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MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
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APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: CUNknown>
CORRESPONDENCE ADDRESS: ADDRESS: BELL, S
                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                           APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
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FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte
STATE: No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BELL,
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                       Johal, Gurmukh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johal, Gurmukh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US20010012886A1th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      John
                                                             CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELTZER,
                                                                                                                                                                                                                                                                                                                                                                                             Score 110; DB 10;
Pred. No. 0.0014;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S P
                                                             AND DISEASE RESISTANCE IN
  PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
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                                                             PLANTS
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-776-491-12
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US-09-776-490-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09776490 Patent No. US20010012886A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 575102 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NQCRHRGMRICRADAGNAKAPTCSYHGWAYDTAG 34
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/810,009
ETLING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                          APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                               CITY: Charlotte
                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                STATE: No.
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/776,491 FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US 08/810,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 919-881-3140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6%;
                                                                                                                                                                                                                                                                           US20010012886Alth Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                     CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 110; DB 10;
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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RESULT 15
US-09-776-491-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09776491
Patent NO. US20010013135A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                         INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 4.5%;
Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NQCRHRGMRICRADGGNAKSPTCSYHGWAYDSAG 34
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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NAME: Spruill, W. Murr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                   NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Charlotte STATE: No. US20010013135Alth Carolina
                                                                                                                                                              TELEX: 575102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELTZER, PARK & GIBSON
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    14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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Gapop 10.0 , Gapext 0.
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2408
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     7799
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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     DB
US-09-004-393B-4
US-09-004-393B-2
US-08-810-009-21
US-08-810-009-21
US-08-810-009-12
US-08-810-009-13
US-08-810-009-13
US-08-810-009-13
US-08-810-009-15
US-08-810-009-19
US-08-810-009-19
US-08-810-009-19
US-08-810-009-10
US-08-810-009-10
US-08-810-009-15
US-08-810-009-17
US-08-810-009-17
US-08-810-009-17
US-08-810-009-17
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US-08-810-009-16
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(without alignments)
1299.432 Million cell updates/sec
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RESULT 2
US-09-004-393B-2
; Sequence 2, Application U;
; Patent No. 6310271
; GENERAL INFORMATION:
; APPLICANT: Hanson D., A

US/09004393B

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; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-004-393B-2
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Best Local Similarity
Matches 58; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/004,393B CURRENT FILING DATE: 1998-01-08 PRIOR APPLICATION NUMBER: 60/035,147 PRIOR FILING DATE: 1997-01-08 NUMBER OF SEO ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Burnet, Michael TITLE OF INVENTION: Polynu TITLE OI INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Briggs,
                                                                                                                                                                                                                                                                                                                                                STREET: r.v.
CITY: Charlotte
CTATE: No. 6211437th Carolina
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TELEPHONE: 919 CC. 1915
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                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                             APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997
                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 FQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYLDSSYHVPYAH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFVGDAYHVGWTH 213
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                                                                          5718-4
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                                                             Matches
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Best Local :
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Best Local
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APPLICANT: Briggs
                                                                                                                                                                                                                                    TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF TRAFFACTORY
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 04-MAR-19
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.V. STREET: P.V. CAITY: Charlotte
CITY: Charlotte
CMATE: NO. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                           / Match 7.2%;
Local Similarity 85.7%;
les 30; Conservative
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                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                         TYPE:
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TOPOLOGY: li
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6211437
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33; Conservative
                                                                                                                                                                                     amino acid
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04-MAR-1997
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94.3%;
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                                                             Score 174; DB 4;
Pred. No. 7.6e-10;
2; Mismatches
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Pred. No. 6.9e-11;
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                                                                                          Length 35;
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RESULT 5 US-08-810-009-21

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Patent No.
GENERAL II
                                                                                                                                                                                                                                                                                                                  Patent No. 6117670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Sequence 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                    NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                                                                                                                                 TITLE OF INVENTION: Pyrrolni TiTLE OF INVENTION: Thereof
                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
   COUNTRY: U
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CENGTH:
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5. 6211437
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                                                                                                                                                                                                                                                                                                                                       5, Application US/09028934
6117670
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: No. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28234
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                                                                                                                                                                                                                                                         Ligon, James M.
Hill, Dwight S.
Lam, Steven T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 amino acids
                                                                                                                                                                                    Kirner, Sabine
Young, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                      van Pee, Karl-Heinz
                                                                                                                                                                                                                                         Hammer, Philip E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                  Pyrrolnitrin Biosynthesis Genes and Uses
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Pred. No. 2.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 35;
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               US-08-810-009-12

; Sequence 12, Application US/08810009

; Patent No. 6211437

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-028-934-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                           327
                                                                                                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                                                                                              267 PELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEV 326
                                                                                                                                                                                                                                                                                                                                                                        207
                                                                                                                                                                                                                                                                                                                                                                                             226 SLAGNAALPPE----GAGLQM-TSKYGSGMGVL-------WDGYSGVHSADLV
                                                                                                                                                                                                                                                                                                                                                                                                                                             161 QSLRFAYETTTSVL----RII------ENFY-DAQHAAPVHQLPISAFELKLFDESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 LEPMFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGE-SIF---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                380 DSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSN 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 LNKKCLGLKEVARVESF-------HGFIYGCFDQEAP----PLMDYLGDAAWY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PVVMERYCSHLGASL-----AKGKVVEGCIQCPFHNWRYDSTGACSHVP-----GHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 IHGDEELFQ-----HELKTIFARNW-LFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/028,934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IHQEPERIRQASGVNDLTTQTAASWYVAMRSDALRGKP---VAIKLFGQPLVAWRDGGGR 61
                                                                                                                                                                                                                      HMLLAIKKG--DGVVRSAANFILYGLQTWAAAGYDVAIWNSMKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRAFLNVCRHRGKTLVSVEAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGES 127
                                                                                                                                                                                                                                                         WTYAIVEKDMPEDLKRRLADSV---QRTLGPAGF----WESDDNDNMETASQNGKKYQSR 379
                                                                                                                                                                                                                                                                                                                                                                    PPPGQEALARDGAWFGAGIDFHVDRYFGPLGVISRTLGLSMSRMQLHFDGYPG-----
                                                                                                                                                                                                                                                                                             -----GCIMTVSLD---GDVKYRL----LQCV---
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Briggs, Steven P.
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149;

Indels 171; Length 379;

Gaps

26;

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-TPVDKEETVM

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225

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RESULT 8
US-08-810-009-14
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Best Local Similarity 52.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14,
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810.000
FILING DATE: 04-MAR-1000
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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NAME: Spruill, W. Murray
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                                                                                                                                                                               CITY: Charlotte
STATE: No. 6211437th Carolina
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TELEPHONE: 919-881-3175
APPLICATION NUMBER: US/0 FILING DATE: 04-MAR-1997
                                                                                                                                                                COUNTRY:
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TELEX: 575102
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6211437
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P.O. Drawer 34009
                                                                                                                                                                  USA
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                                                                                                                                                                                                                                          BELL,
                                                                                                                                                                                                                                          SELTZER, PARK & GIBSON
                   us/08/810,009
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Pred. No. 0.0009;
4; Mismatches 12;
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US-08-810-009-13
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US-08-810-009-13
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Query Match
Best Local Similarity
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TELEX: 575102
INFORMATION FOR SEQ ID NO:
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TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 919-881-3140
                                                                    MOLECULE TYPE:
                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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STREET: P.U. -
CITY: Charlotte
STATE: NO. 6211437th Carolina
                                                                                                                                                                                      TELEPHONE: 919-00-
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                                                                                   STRANDEDNESS:
TOPOLOGY: li
                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                FILING DATE: 04
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 919 C. TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                 NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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REFERENCE/DOCKET NUMBER: 57
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                                                                                                                                   LENGTH:
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                                                                                                                  amino acid
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                                                                                                                                    35 amino acids
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                                                                                     linear
                                                                  protein
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   4.5%;
52.9%;
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Pred. No. 0.0011;
   Score 108; DB 4; Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
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                  Length 35;
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RESULT 11
US-09-311-626B-4
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                                                        GENERAL INFORMATION:
APPLICANY: JOrgensen, Per Lina
APPLICANY: Schnorr, Kirk
APPLICANT: Andersen, Lene No. 6399347boe
APPLICANY: Schulein, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Described in September 15, Application US/08810009 Patent No. 6211437
                                                                                                                                               Sequence 4, Application US/09311626B Patent No. 6399347
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           Matches
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             APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MUTRAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/311,626B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                            79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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Patent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurnukh S.
APPLICANT: Gray, John
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Best Local
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PRIOR APPLICATION NUMBER: 0608/98
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: 60/084,358
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                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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                  APPLICATION NUMBER: FILING DATE: 04-MAR
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ZIP: 28234
                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                            STREET: P.O. Dr. CITY: Charlotte
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                  JMBER: US/08/810,009
04-MAR-1997
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21.6%;
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US-08-810-009-18
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     Matches
                  Best
                                Query Match
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                                                                                                                                                                        TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Joha, Gurmukn J.

APPLICANT: Gray, John
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
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LENGTH: 35 amino acids
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                                                                                  MOLECULE TYPE:
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STREET: F.C.
CITY: Charlotte
CTATE: NO. 6211437th Carolina
                Local
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                                                                                                STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                                                                                                                                            NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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TOPOLOGY: li
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REFERENCE/DOCKET NUMBER:
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   Conservative
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Score 104; DB 4; Length 35; Pred. No. 0.0033; Indels 14; Indels
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Pred. No. 0.0022;
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US-08-809-326A-16
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GENERAL I
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TELEX: 66141 PE
INFORMATION FOR SEQ
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
MOLECULE TYPE:
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 74: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: JP 1:
FILING DATE: 28-APR-1995
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                                  LENGTH: 432 amino acids TYPE: amino acid
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FILING DATE: 28-APR-1995
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10036-2711
                                                                                                                                                                                                                                  Miller, Charles
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                                                                                                                                    (212) 869-8864/9741
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Matsumoto, Akira
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                      linear
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                                                                                                 ID NO:
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FISSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
FIGSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
DREASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
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Best Local Similarity
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                                                       CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: JP 224711/94

FILING DATE: 20-SEP-1994

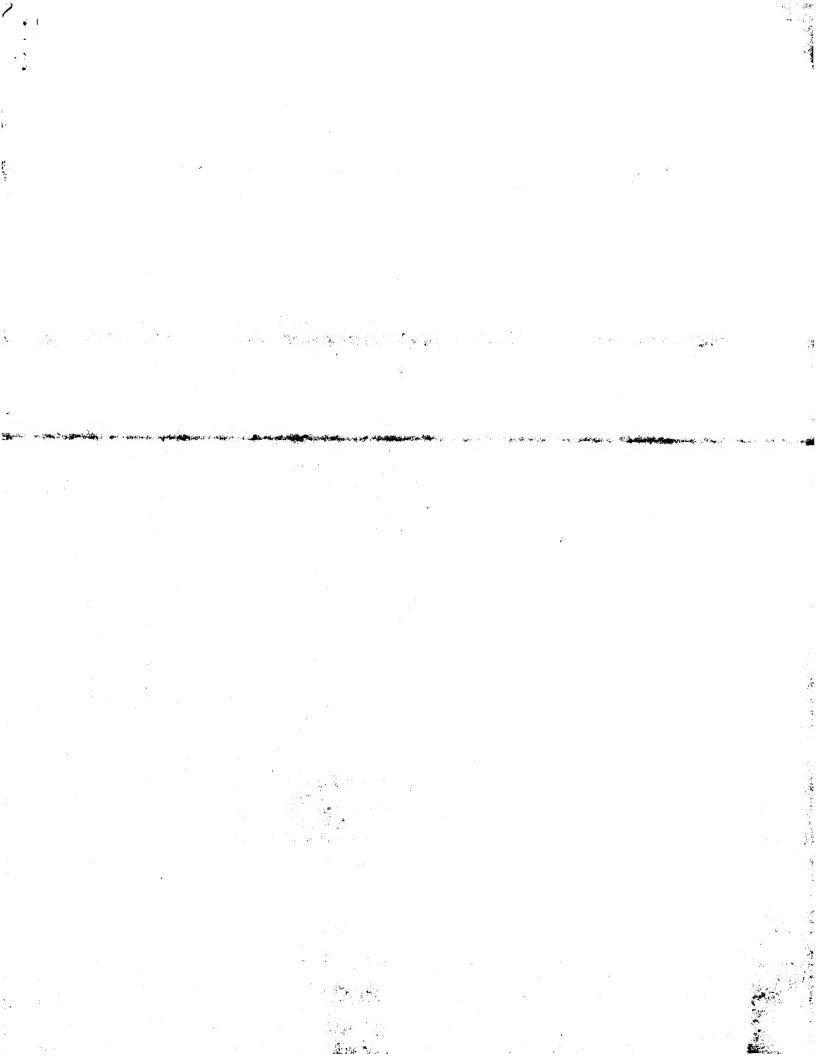
PRIOR APPLICATION NUMBER: JF 106006/95

FILING DATE: 28-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 106008/95

PRIOR APPLICATION NUMBER: JP 106008/95
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                     PRIOR APPLICATION DATA:
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COUNTRY:
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                                             FILING DATE:
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6165478
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1155 Avenue of the Ameri
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Matsumoto, Akira
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                                          28-APR-1995
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19-MAR-1997
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21.4%;
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSTS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OF
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
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JP 106009/95
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Pred. No. 0.17;
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Search completed: January 27, 2003, 09:04:56 Job time: 11.1667 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                              171
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                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                       195 WKAPAENFVGDAYHVGWTHASSL-----RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
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                                                                                                                                                                                                                                                                                                                         22 WNLPAD------LAWFKRNTLNKPVIMGRHTWESIGRPLPGR-----KNIILSSQP 66
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                                                               KDKTSSTT
                                                                                                                                                                                                                                                          GTDDRVTW-----VKSVDEAIAACGDVPEIMVIGGG---RVYEQFLPKAQKLYLTHIDAE 118
                                                                                              KSAIGETS 412
                                                                                                                            -----DNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAGASG
                                                                                                                                                          AGFWESDDNDNME----TASQNGKKYQSRDSD-----LLSNLGFGEDVYGDAVYPGVVG
                                                                                                                                                                                         VEGDTHFPDYEPDDWESVFSEFHDADAQNSHSYEFEILE-----
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21.4%; Pred. No. 0.32;
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Title:
Perfect score:
Sequence:
Re
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                  SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_mammal:*
7: sp_mhc:*
7: sp_mhc:*
8: sp_organelle
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebras:
14: sp_unclass:
15: sp_nacteri:
16: sp_bacteri:
16: sp_archeap:
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Gapop 10.0 , Gapext 0.5
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1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449
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sp_bacteria:*
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sp_plant:*
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                                     SUMMARIES
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No.	Score	Query Match	Query Match Length DB	BIG	ID	Description
ц	2332	96.8	449	2	Q938R9	Q938r9 pseudomonas
2	2292	95.2	449	N	Q52142	
ω	2208	91.7	449	Ν	Q9ZI73	
4	2193	91.1	447	Ν	Q9L5D2	N
ហ	2189	90.9	447	N	052382	
თ	2072	86.0	447	N	Q8VUD4	
7	2054	85.3	447	2	P95564	
8	2025	84.1	447	N	Q8RTL4	
9	1967.5	81.7	451	2	Q45695	Çī.
10	1490	61.9	277	N	Q9ETK2	
11	1488	61.8	277	N	Q9F5S4	
12	1486	61.7	277	N	Q9F5T3	-
13	1484	61.6	277	N	Q9F5S8	œ
14	1483	61.6	277	N	Q9F5S9	9
15	1451	60.3	277	2	Q9F5S3	
16	1405	58.3	277	Ν	Q9EUC7	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
1002	1009	1016	1038	1038	1039	1040	1045.5	1067	1113.5	1123	1127	1134	1134	1139	1355.5	1384	1390	1393	1393	1393	1393	1393	1396	1396	1399	1399	1402	1403
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Ν	N	N	N	2	Ν	N	N	N	Ν	Ν	N	2	N	2	Ν	N	N	N	N	N	N	N	2	Ν	2	N	N	2
Q93M41	Q93M39	Q93M40	Q8VUM2	Q8VR21	Q8VUM5	Q9F6B6	Q9WXG8	Q8VR25	Q93NA8	Q8VR22	Q8VR24	Q8VL21	Q8VR23	Q8VUM6	Q9ZHH3	Q9F5S2	Q9F5T7	Q9F5S6	Q9F5T0	Q9F5T1	Q9F5T2	Q9F5T4	Q9F5S7	Q9F5T6	Q9F5S5	Q9ETV3	Q9F5T5	Q9F5T8
Q93m41 uncultured	unculture	uncultured	ralstonia										pseudomona	ralstonia		Q9f5s2 pseudomonas			Q9f5t0 pseudomonas								טי	Q9f5t8 pseudomonas

ALIGNMENTS

Qy	Qy Db	Qу ДЬ		SQ	DR	DR	DR	DR	DR	RL	RA	RP	RN	ox S	8	8	SO	GN	DE	DT	Dī	DI	AC	ID	Q9
121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 	1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60 	Query Match 96.8%; Score 2332; DB 2; Length 449; Best Local Similarity 96.0%; Pred. No. 1e-171; Mismatches 431; Conservative 12; Mismatches 6; Indels 0; Gaps	SEQUENCE 449 AA; 49608 MW; 5EFEDBE0282FE812 CRC64;	PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.	<pre>pfam; pF00848; Ring_hydroxyl_A; 1.</pre>	InterPro;		EMBL; AY048759; AAL07262.1;	Submitted (OCT	Min KH				Pseudomonas.			NAHAC.	Naphthalene dioxygenase.	01-MAR-2002 (TrEMBLrel. 20, Last	01-DEC-2001 (TrEMBLrel. 19,	01-DEC-2001 (TrEMBLrel.	Q938R9;	Q938R9 PRELIMINARY; PRT; 449 AA.	RESULT 1 Q938R9

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        EMBL; AB00400,
HSSP; P23094; 1NDO.
InterPro; IPR001281; Rieske.
InterPro; IPR00168; Ring_hydroxyl_A.
R Pfam; PF00355; Rieske; 1.
JR Pfam; PF00848; Ring_hydroxyl_A; 1.
DR PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
449 AA; 49361 MW; 80020F54AAB11E8A CRC
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Best Local :
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052142; 008194;
01-NOV-1996 (Tre
01-NOV-1996 (Tre
01-DEC-2001 (Tre
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OUS82.";
                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification and characterization of genes encoding po
aromatic hydrocarbon dioxygenase and polycyclic aromatic
dihydrodiol dehydrogenase in Pseudomonas putida OUS82.";
J. Bacteriol. 176:2444-2449(1994).
                                                                                                                                                                                                                              Submitted (JUN-1997) to the EMBL; AB004059; BAA20391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-OUS82;
Takizawa N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94209249; PubMed-8157615; TAKIZAWA N., Kaida N., Torigoe S.,
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Au W., Masao F., Hohzoh K.,
Molecular analysis of NAH7-type
mosomes of Pseudomonas aeruginos
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on update)
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                   Gene 236:149-157(1999).
EMBL; AF03953; AADO2136.1; --
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InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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SEQUENCE (
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99365311; PubMed=10433976;
Bosch R., Garcia-Valdes E., Moore E.R.B.;
"Genetic characterization and evolutionary implications of
                                                                                                                                                                                                                                                                                                                                                        chromosomally encoded naphthalene-degradation Pseudomonas stutzeri AN10.";
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EMBL; AF25550; AAF72976.1; -
HSSP, P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR00163; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Insights into the genetic diversity of degrading bacteria.";
Appl. Microbiol
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Q9L5D2;
01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Polyaromatic hydrocarbon dioxygenase large subunit.
                                                                                                                                                                                                                                                                                                        Dioxygenase
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Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
                                                                                                                                                                                                                                                                                                                                      PROSITE;
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88.9%;
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Pred. No. 5.5e-161;
27; Mismatches 21;
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RINC_HYDROXYL_ALPHA;
                                                                                                                                                                     MEDLINE=20576173; PubMed=11133965;
Zhou N.Y., Fuenmayor S.L., Williams P.A.;
"nag genes of ralstonia (Formerly pseudomonas)
enzymes for gentisate catabolism.";
J. Bacteriol. 183:700-708(2001).
                                                                                                                                                                                                                                                                     MEDLINE=98233751; PubMed=9573207;
Fuenmayor S.L., Wild M., Boyes A.L., Williams
"A gene cluster encoding steps in conversion
gentisate in Pseudomonas sp. strain U2.";
D. Bacteriol. 180:2522-2530(1998).
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                                                   SEQUENCE
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                                                                                                                                                EMBL; AF036940; AAD12610.1; HSSP; P23094; 1NDO.
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Score 2189; DF Pred. No. 1.1e-25; Mismatches
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                                                                        Johnson G.R., Jain R.K., Spain J.C.;
"Origins of the 2,4-dinitrotoluene pathway.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF169302; AAL50021.1; -.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Rieske.
InterPro; IPR001663; Rieske; 1.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PFAINTS; PR00090; RNGDIOXGNASE;
PRINTS; PR00090; RNGDIOXGNASE;
PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.
SEQUENCE 447 AA; 49468 MW; 2A5BF8558320275C CRC64;
                        Query Match
Best Local Similarity
Matches 375; Conser
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Q8VUD4;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Burkholderia cepacia (Pseudomonas cepacia).
Proteobacteria; beta subdivision; Burkholderia
                                                                                                                                                                                                                                                                                   Johnson G.R., Jain R.K., Spain J.C.; "Properties of the trihydroxytoluene oxygenase cepacia R34: an extradiol dioxygenase from the pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Burkholderia.
                                                                                                                                                                                                                             STRAIN-R34;
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MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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(TrEMBLrel.
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Last sequence up
Last annotation
                       Score 2072; DB 2;
Pred. No. 1.2e-151;
9; Mismatches 33;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
SEQUENCE 447 AA; 49485 MW; ICBOE223
                                                                                                                                                                                                                                                                                                                                                                                                                dioxygenase from pseudomonas sp. JS42.";
Gene 18:57-61(1996)
EMBL; U49504; AA840383.1;
HSSP; P23094; INDO.
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=306;
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                                                                                   MSYQN--LVSEAGLTQKLLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVTAKMG
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01-JUN-2002 (TrE)
01-JUN-2002 (TrE)
Oxygenase-alpha |
                                                                                                                                                                                                                                                                             MEDLINE=21681044; PubMed=11823201;
Lessner D.J., Johnson G.R., Parales R.E., Spain J.C.,
"Molecular Characterization and Substrate Specificity
Dioxygenase from Comamonas sp. Strain JS765.";
Appl. Environ. Microbiol. 68:634-641(2002).
EMBL; AF379638; AAL76202.1; -
EMBL; AF379638; AAL76202.1; -
SEQUENCE 447 AA; 49556 MW; 4CA961F99A37DF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                STRAIN=JS765;
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=58226;
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QMTSKYGSGMGVFWGYYSGNESADMIPDLMAFGAAKQEKLAKEIGDVRARIYRSFLNGTI
            QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                       ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                    IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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                                                                                                                                       VDEVIVSRQNDGSVRAFLNVCRHRGKTLVHAEAGNAKGFVCGYHGWGYGSNGELQSVPFE
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368; Conser
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Proteobacteria;
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82.0%;
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Pred. No. 5.1e-148;
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Best Local :
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045695;
01-NOV-1996
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Burkholderia.
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPH;
PROSITE; PS00570; RING_HYDROXYL_ALPH;
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EMBL; U62430; AAB09766.1;
HSSP; P23094; INDO.
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"2,4-Dinitrotoluene dioxygenase from Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96326338; PubMed=8759857;
Suen W.C., Haigler B.E., Spain J.
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DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                      FPNNCFLTGAGVFKVFNPIDENTTEAWTYAIVEKDMPEDLKRRLADAAQRSTGPAGYWES
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451 AA; 49827 MW; 726796C29CEF9A10 CRC64;
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Best Local Similarity
Matches 277; Conserv
Q9F5S4;
Q9F5S4;
01-MAR-2001
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00099; RNGDIOXGNASE.
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Pred. No. 4.9e-107;
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01-MAR-2001
01-MAR-2001
01-DEC-2001
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NON_TER
NON_TER
2
SEQUENCE 27
                                                                              SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=139738
                                                                                                                               Pseudomonas
                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                             Pseudomonas
                                                                                                                                                                                NAHAC
                                                                                                                                                                                              Naphthalene
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Pfam; PF00848; Ring_hydroxyl_A;
PRINTS; PR00090; RNGDIOXGNASE.
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InterPro; IPR001663; Ring_hydroxyl_A.
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277 AA;
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99.6%;
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STRAIN=10IIDNH;
STRAIN=10IIDNH;
Ferrero M.A., Lalucat J., Bosch R.;
Coexistence of two naphthalene dioxygenase genes
Pseudomonas strains from West Mediterranean Sea.";
Pseudomonas strains from West Mediterranean Sea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase genes
Pseudomonas strains from West Mediterranean Sea.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
invagenase iron sulfur protein (Fragment).
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No. 7e-107;
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Best Local :
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SEQUENCE
                                                                                                                                           "Coexistence of two naphthalene dioxygenase genes (naha "Coexistence of two naphthalene dioxygenase genes (naha Pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF306434; AAG25694.1; ...
                                                                                                                                                                                                                                                                                                               Q9F5S8;
01-MAR-2001
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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01-DEC-2001
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InterPro; IPR001663; Ring_hydroxyl_A.
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Bacteria; Proteobacteria;
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P23094; 1NDO.
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                                                                      RING_HYDROXYL_ALPHA;
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Pred. No. 1e-106;
0; Mismatches
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1484; DB 2;
No. 1.4e-106;
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protein (Fragment).
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Matches 276
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Q9F5S9;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                               Dioxygenase.
NON_TER
NON_TER
SEQUENCE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                            SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
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                                               HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
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Best Local Similarity 96.8%;
Matches 268; Conservative
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SEQUENCE 277
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00099; RNGDIOXGNASE.
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"Coexistence of two naphthalene dioxygenase genes (nahAc)
"Coexistence of two naphthalene dioxygenase genes (nahAc)
"Coexistence of two naphthalene dioxygenase genes (nahAc)
"Seculomonas strains from West Mediterranean Sea.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR306441; AAG25701.1; -...
HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Naphthalene dioxygenase iron sulfur protein 1 (Fragment).
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                                                                                                     LNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIV 332
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                       27,
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Pred. No. 5e-104;
6; Mismatches 3;
                       09:02:23
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OM protein - protein search, using sw model
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Title:
Perfect score:
Sequence: US-09-843-250-35 2408 1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449 January 27, 2003, 08:47:32; Search time 7.16667 Seconds (without alignments) 2598.540 Million cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 112892

112892 seqs, 41476328 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	σι	υī	4	ω	2	1	Result
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POLN_HEVBU	AGLU_ASPOR	SGT1_ARATH	LOL2_HUMAN	SYC_AERPE	SYI_STAAU	DHE3_PYRKO	POLN_HEVMY	ORP8_HUMAN	ATPA_ENTHR	F26_YEAST	UNRI_HUMAN	
P29324	Q12558	Q91sm5	Q9y4k0	Q9ybk6	P41972	059650	Q04610	Q9bzf1	P26679			
hepatitis e	aspergillus	arabidopsis	homo sapien	aeropyrum p	staphylococ	pyrococcus	hepatitis e	homo sapien	enterococcu	saccharomyc	homo sapien	

ALIGNMENTS

R R R R R R R R R R R R R R R R R R R	RESULTION OF PROCESSION OF PRO
SEQUENCE FROM N.A. SPECIES-P. putida; STRAIN=NCIB 9816; Parales J.V., Parales R.E., Kumar A., Gibson D.T.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. SIRAIN=C18; SEQUENCE FROM N.A. STRAIN=C18; MEDLINE-94042852; PubMed=8226631; Denome S.A., Stanley D.C., Olson E.S., Young K.D.; MEDLINE-94042852; PubMed=8226631; Denome S.A., Stanley D.C., Olson E.S., Young K.D.; Metabolism of dibenzothiophene and naphthalene in Pseudomonas strains: complete DNA sequence of an upper naphthalene catabolic pathway."; J. Bacteriol. 175:6890-6901(1993). SEQUENCE FROM N.A. SPECIES-P. putida; STRAIN=G7 / ATCC 17485; PLASMID=NAH7; SEQUENCE FROM M.J., OSSLUND T.D., Saunders R., Ensley B.D., Suggs S., SIMON M.J., OSSLUND T.D., Saunders R., Ensley B.D., Suggs S., Harcourt A.A., Suen WC., Cruden D.L., Gibson D.T., Zylstra G.J.; "Sequences of genes encoding naphthalene dioxygenase in Pseudomonas putida strains G7 and NCIB 9816-4."; Gene 127:31-37(1993). SEQUENCE FROM N.A. SPECIES-P. putida; STRAIN=BS202; PLASMID=NPL1; Bezborodnikov S.G., Boronin A.M., Tiedje J.M.; "Nucleotide sequences of genes encoding an upper pathway of naphthalene metabolism of NPLI plasmid from Pseudomonas putida strain Sydbmitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.	PSEPU PSEPU PSEPU PSEPU PSEPU PSEPU O1-NOV-15

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InterPro; IPR001663; Ring_hydroxyl_A.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreo
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-I - FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
-I - FUNCTION: COMPONENT ON STATEM WHICH CATALYZES THE INCORPORATION BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CISNAPHTHALENE DIHYDRODIOL.
-I- CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1,2-dihydronaphthalene-1,2-diol + NAD(+).
                                                                                                                                                                                                                                                                                                            PDB;
                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                  Dioxygenase;
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS). SPECIES-P.putida; STRAIN-NCIB 9816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. SPECIES=P.putida; STRAIN=ATCC 17484;
                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of an aromatic-ring-hydroxylating dioxygenase-naphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98298434; PubMed-9634695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. PATHMAY: UPPER NAPHHALENE CATABOLIC PATHMAY WHICH INVOLVES CONVERSION OF NAPHHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHLOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO LICHTOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO CATE AND THE METABOLISM OF DBT IS LIMITED TO CATE AND THE AROMATIC RING.

SUBUNIT: NAPHHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT IS COMPOSED OF SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN RODOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS COMPOSED OF AN HEXAMER OF THREE LARGE ALPHA SUBUNITS (NDOB) AND THREE SMALL BETA SUBUNITS (NDOC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
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Hamann C.;
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5-DEC-1998 (Rel. 37, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
aphthalene 1,2-dioxygenase alpha subunit (EC,2-dioxygenase ISP alpha).
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PROSITE; PS00570; RING_HYDROXYL_ALPHA;
Aromatic hydrocarbons catabolism; Oxid
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InterPro: IPR001663; Ring_hydroxyl_A.
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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COFACTOR: PROBABLY BINDS A 25E-2S GROUP AND AN IRON ATOM.

PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES

CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF

DIBENZOTHIOPHENE (DET) AND PHENANTHRENE. CONVERTS PHENANTHRENE

1-HYDROXY-2-NAPTHOLY ACID AND THE METABOLISM OF DET IS LIMITED

OXIDATION OF THE AROMATIC RING.
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SIMILARITY:
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HSSP; P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-:- FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION
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the chromosome of Pseudomonas aeruginosa PaK1.
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Best Local S
Matches 403
                                                                    SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloc
Blattner F.R., Plunkett G., Glasner
Riley M., Collado-Vides J., Glasner
                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-phenylpropionate dioxygenase alpha subunit (Digoxigenin alpha subunit)
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METAL
SEQUENCE
                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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01-NOV-1997 (Re
                                                                                                                                                 Turlin E., Gasser F.,
Submitted (SEP-1994):
                                                                                                                                                                                                                                                  Escherichia coli, and Escherichia coli 0157:H7
  SEQUENCE
                                                                                                                                                                          STRAIN-K12;
                                                                                                                                                                                                              NCBI_TaxID=562,
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                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - K12 genome corresponding to 50.0-6 analysis of its sequence features."; DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Ison Itoh T., Kimura S., Kitagawa M., Makimo K., Miki T., Mits Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivas Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K
                                          PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                    EcoGene; EG13456; hcaE.
InterPro; IPR001281; Rieske.
InterPro; IPR001653; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21074935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=0157:H7
                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of enterohaemorrhagic Escherichia
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- K12 genome corresponding to 50.0-68
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                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                        D90883; BAA16433.1; -. D90884; BAA16441.1; -. AE005484; BAG57651.1; -. AP002562; BAB36827.1; -.
                                                               PF00848; Ring_hydroxyl_A; s; PR00090; RNGDIOXGNASE.
                                                                                                                                P23094; 1NDO.
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PubMed=11206551;
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Best Local S
Matches 165
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                                                 Tan H.-M., Tang H.-Y., Joannou C., Abdel-Wahab N.H., "The Pseudomonas putida ML2 plasmid-encoded genes for dioxygenase are unusual in codon usage and low in G+Gene 130:33-39(1993).
                                                                                                           SEQUENCE FROM N.A.,
STRAIN=ML2;
                                                                                                                                                                                  Plasmid
                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last ann
Benzene 1,2-dioxygenase alpha
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01-NOV-1995
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           CATALYTIC ACTIVITY: Benzene + NADH + O(2) = dihydrobenzene-1,2-diol + NAD(+).
COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND
  COFACTOR: PROB
PATHWAY: FIRST
                                                                                                                                                                                                                                                                                                                                            ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
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YQRWADLLSSESWQEVLDKTAAYQQEVMK -> ATAPATAN
CVWKWGLVRKSAATTAFLALLTISFQKLPLVECTNAGPIF
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                                                                                                                                                                                                                    notation update) subunit (EC 1.14.12.3).
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PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
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use by non-profit institutions as long as its content
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SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                         AHVSSSNW
                                                                                                                  PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWESD
                                                                                                                                                                      WDGY-SGVHSAD-----LVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVF
                                                                                                                                                                                                                                                                                                                        KMMTSPDW
                                                 DGENWVEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
                                                                       DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ
                                                                                                                                                   {\tt WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF}
                                                                                                                                                                                                                                WKAPAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
                                                                                                                                                                                                                                                         PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
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                                                                                                 PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
                                                                                                                                                                                                       WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP------
                                                                                                                                                                                                                                                                                 ~-VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
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IRON-SULFUR (2FE-2S) (:
IRON-SULFUR (2FE-2S) (:
IRON-SULFUR (2FE-2S) (:
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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Pred. No. 7.4e-
59; Mismatches
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Pfam; PF00
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01-JAN-1990 (Rel. 13, La
15-JUN-2002 (Rel. 41, La
Toluene 2,3-dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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J. COFACTOR: PROBABLY BINDS A 2FE-2S GROUP
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00090; RNGDIOXGNASE PROSITE; PS00570; RING_HYDROX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A36516; A36516
HSSP; P23094; 1NDO.
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PIR; A36516; A36516.
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Pseudomonas
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SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTE
TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (TODC1 AND TO)
FERREDOXIN (TODB) AND A FERREDOXIN REDUCTASE (TODA).
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
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                                                                                                                                            VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE---
                                                                                                                                                                                                  IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
VLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                        WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                                 WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                             PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                                    --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                 QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
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PF00848; Ring_hydroxyl_A; 1.
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145; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                Haddock J.D., Gibson D.T.;
Haddock J.D., Gibson D.T.;
"Purification and characterization of the
biphenyl 2,3-dioxygenase from Pseudomonas
J. Bacteriol. 177:5834-5839(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BPHA_BURCE P37333;
                                                                                                                                                                                      This SW
between
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15-JUN-2002 (Rel. 41, Last annotation update)
Biphenyl dioxygenase alpha subunit (EC 1.14.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BURCE
                                                                                          entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polychlorinated-biphenyl-degrading enzyme LB400.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erickson B.D., Mondello F.J.;
"Nucleotide sequencing and transcriptional mapping encoding biphenyl dioxygenase, a multicomponent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=292;
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Burkholderia.
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                                                                                                                 modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 174:2903-2912(1992).
                                                                                                                                                          s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                            BphE subunits. A ferredoxin (BphF) and a ferredoxin red (BphG) must be present to obtain activity. SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                 SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                      first step.
                                                                                                                                                                                                                                                      DIOXYGENASE ALPHA SUBUNIT FAMILY.
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                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429
                                                                                                               non-profit institutions as long and this statement is not removed.
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subdivision;
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                                                                                                                             ng as its content
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                                                                                       http://www.isb-sib.ch/announce/
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                                                                                                               Usage
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PIR; B41858; EMBL; M86348; or send

B41858

AAB63425.1;

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HA_COMIE

DEPHA_COMIE

O46372;

C Q46372;

T 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

Riphenyl dioxygenase alpha subunit (EC 1.14.1
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                                                                     Comamonas
Bacteria;
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INIT_MET
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PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Risske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
            STRAIN=B-356;
MEDLINE=97045812;
 Sylvestre
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                                   SEQUENCE FROM N.A.
                                                          NCBI_TaxID=285;
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PubMed=8890734;
ois M., Hurtubise
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                                                                     (Pseudomonas testosteroni)
ia; beta subdivision; Comam
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IRON (BY SIMILARITY).
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Pred. No. 4.3e-41;
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                                                                                                                   on update)
(EC 1.14.12
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 Bergeron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biphenyl/chlorobiphenyl dioxygenase genes: evolutionary among Gram-negative bacterial biphenyl dioxygenases."; Gene 174:195-202(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shareck F., Barriault D., Guillemette I., Juteau "Sequencing of Comamonas testosteroni strain B-35"
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dioxygenase;
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00090; RNGDIOXGNASE.
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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J. Biol. Chem. 267:4844-4853(1992)
-i. CAPALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-i. COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit (B)
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15-JUN-2002 (Rel. 41, Last ann)
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between the Swiss Institute of Bioinformatics and the EMBL outst
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InterPro; IPR001663; Ring_hydroxyl_A.
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15-JUL-1999
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Irie S., Doi S., Yorifuji T., Takagi M., Yano K.;
"Nucleotide sequencing and characterization of the genes encodin benzene oxidation enzymes of Pseudomonas putida.";
J. Bacteriol. 169:5174-5179(1987).
-!- CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-dihydrobenzene-1,2-diol + NAD(+).
-!- CATACTRIC PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP ENZENE TO CATECHOL.
-!- PATHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.
-!- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS:
TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BUZA AND BNZB), A
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                                                              European Bioinformatics Institute.
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                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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  Horriuchi H., Take
"Identification (
KKS102 involved
Fukuda M., Yasukouchi Y., Kikuchi Y., Nagata
Horiuchi H., Takagi M., Yano K.;
"Identification of the bphA and bphB genes of
KKS102 involved in degradation of biphenyl ar
                                                                                  SEQUENCE FROM N.A. MEDLINE=94324977; PubMed=8048958;
                                                                                                                                                               Pseudomonas sp. (strain F
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InterPro; IPR001663; Ring_hydroxyl_A.
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Pfam; pF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00909; RNGDTOXGNASE.
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Best Local S
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METAL 1
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METAL 2
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SEQUENCE 45
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Biphenyl-polychlorinated biphenyl degradation pathway;
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                                             AGGTFEQDDGENWVEIQRGLRGHKAKSAPLCAQMGLNVPNKSNPDFP----GKTAYVYAEE
                                                                                    PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGET
                                                                                                                                                                                NCTVFPNNSMLTCSGVFKVWNPIDANTTEV---WTYAIVEKDMPEDLKRRLADSVQRTLG
                                                                                                                                                                                                                             SQFRAAWGGHGSGWFINDAAILMAVMGPKTTQYWTQGPAAEKAAKRLNQMPTQTMFGQHM
                                                                                                                                                                                                                                                                           SGMGVLWDGYSGVHSADLVPELMAFGGAK-----QERLNKEIGDVRAR-IYRSHL
                                                                                                                                                                                                                                                                                                                         CNWKFAAEQFCSDMYHAGTMAHLSGVLS-----SLPPE---MDLTQVQMSKNG
                                                                                                                                                                                                                                                                                                                                                                    ANWKAPAENFYGDAYHYG-WTHASSLRSGESIFSSLAGNAALPPEGAGLQMT----SKYG
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147; Conser
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nilarity 33.6%;
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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XYLX_PSEPU
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01-NOV-1991
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92155191; PubMed=1740120;
MEDLINE-92155191; PubMed=1740120;
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METAL
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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                                                                                                                                                                                                                                                                                                                                                       METAL
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InterPro; IPR001663; Ring_hydroxyl_A.
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J. BIOCHEM. 204:113-120(1992).

COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. COFACTOR: DEGRADATION OF BENZOATE AND TOLLATE TO CATECHOL. SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEINS: TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (XYLX AND XYLY), ALELECTRON TRANSFER COMPONENT (XYLZ).

SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
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                          HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKKCLG---LKEV
HRGATLCRFRSGNKATHTCSFHGWTFSNSGKLLKVKDPKGAGYPDSFD--CDGSHDLKKV
                                                                                     DPRLEDLEMKHIFEGNWIYLAHESQIPEKNDYYTTQMGRQPIFITRNKDGELNAFVNACS
                                                                                                                               DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
                                                                                                                                                                                                         Similarity
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nilarity 31.2%;
Conservative 6
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(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)
(rel. 37, Last annotation update)
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IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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1; Mismatches
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Pred. No. 7.
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15-JUN-2002
15-JUN-2002
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                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXONASE.
PROSITE; PS00570; RING_HYDROXYL_ALI
                                                                                                                                                                      modified
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on i
Aromatic hydrocarbons catabolism; Oxidoreductase; Iron-sulfur; Iron;
                                                              PIR; S234//; S234//.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                               EMBL; AF009224; AAC46436.2; PIR; S23477; S23477.
                                                                                                                                                                                    use
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 84; 103-104; 171-172 AND Elby D.M., Neidle E.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for benzoate 1,2-dioxygenase reveal multicomponent oxygenases.";
J. Bacteriol. 173:5385-5395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neidle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BD413 / ADP1;
MEDLINE=91358314; PubMed=1885518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BD413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P07769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequences of the Acinetobacter calcoaceticus benABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acinetobacter calcoaceticus
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                                                                                                                                                                                                                                                                                                 COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
PATHWAY: DEGRADATION PATHWAY LEADING FROM BENZOATE TO CATECHOL.
SUBUNIT: THIS DIGYCENASE SYSTEM CONSISTS OF THREE PROTEINS: TH
TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BENA AND BENB), AND
                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Benzoate +
                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE BACTER: DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                    AN ELECTRON TRANSFER COMPONENT (BENC) SIMILARITY: BELONGS TO THE BACTERIAL
                                                                                                                                                                                                                                                                                                                                                            NAD(+)
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                                                                                                                                                                     and this statement is not removed.
                                                                                                                                                                                    non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 20, Created)
(Rel. 41, Last sequence up
(Rel. 41, Last annotation
                                                                                             S23477
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             RING_HYDROXYL_ALPHA;
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SEQUENCE
                                                                   STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Pern Riley M., Collado-Vides J., Glasner J.D., Rode C Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative dioxygenase alpha subunit yeaw (EC 1
YEAW OR B1802 OR Z2845 OR ECS2511.
                                                                                                                         SEQUENCE FROM N.A. STRAIN-K12 / MG165
                                                                                                                                                                                                 Escherichia coli, and Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                    ECOLI
          SEQUENCE
                                   Science
                                            "The
                                                                                                                                                                           Escherichia
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                                                            B., Shao Y.;
                                  complete genome sequence of nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLELVGPPGKVVIKANWKAPAENFVGDAYHVG---WTHASSL-----RSGESIFSSLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKILV--SESGLSQKH-LIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGI 61
                                                                                                                                                                                                                                                                                                                                                                                          ---VYPGVVGKSAIGETSYRGFYRAYQAHVSSSNWAEFEHAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWG---KHGGG-----SYGFEHGHMLLWTQWGNPEDRPNFPKAAEYTEKFGAAMSKWM---
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IRON-SULFUR (2FE-2S) (I
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IRON (BY SIMILARITY).
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Pred. No. 6.
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                       subdivision;
                                              Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                      374
                                                                               .A., Perna N.T., Burl
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.5e-24;
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) (BY SIMILARITY).
                                                                       Rose
                                                                               , Burland V.,
                                                                       D.J.,
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DP 6A

DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR 82

DQNAFEHEKENVFAKSWICVAHSSELANANDYVTREIIGESIVLVRGRDKVLRAFYNVCP

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STETTTERS ARABARA RABARA RABARA RABARA RABARA KODO COCOCOCOCOCOCO RABARA      Query Match
Best Local S
Matches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000274; AAC74872.1; -.
EMBL; D90823; BAA15597.1; ALT_INIT.
EMBL; D90824; BAA15606.1; ALT_INIT.
EMBL; AE005403; AAG56791.1; -.
EMBL; AP002558; BAB35934.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe 1 Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunae R., Shiba T., Hattori M., Shinagawa H.; Ruhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparatison with a laboratory strain K-12."; DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C Yamamoto Y., Horiuchi T.; Yamamoto Y., Horiuchi T.; R460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage manna Res. 3:379-392(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene; EG13509; yeaW.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T. Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Mizobuchi K., Mori H., Mori T., Saito N., Sampei G., Seki Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=015/:H/ / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=0157:H7 / R
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                                                                                                                                                                                                                                                                                                                               PROSITE; PS00570; RING_HYDROXYL_ALPHA;
Hypothetical protein; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00355; Rieske;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATON SUBUNIT: PROBABLE HETERODIMER OF YEAW AND YEAX. SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                      Complete
        l Similarity
99; Conser
                                                                                                    te proteome.

89 89

91 91

109 109

112 112

211 211

216 216

374 AA; 425
        Conservative
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                                                                                                                  42561 MW;
                              10.4%;
        53;
Score 251; DB Pred. No. 2.1e-53; Mismatches
                                                                                                                                   IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON (BY SIMILARITY).

IRON (BY SIMILARITY).
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                              251;
No. 2.
                                                                                                                                                                                                                                                                                                                               Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                           FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli 0157:H7.";
        DB 1; I
1.1e-12;
les 126;
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                                                        Length 374;
                                                                                                                  CRC64;
        Indels
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, Miki T.,
Nakamura Y.,
                                                                                                                                                                                                                                                                                                                               Dioxygenase;
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           90;
     Gaps
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RESULT 15

CHMO_AMATR
ID CHMMO_A
AC Q93XE1
DT 15-JUN
CMO.

OS Amaran
OC Sperma
OC SPERMA
CATISSUE
RX MEDLIN
RR MEDLIN
RA Meng Y
RT 1:ICO1
RL Cell R
CC -!- FU
CC -!- SU
CC -!- S
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15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meng Y.L., Wang Y.M., Zhang B., Nii N.;
"Isolation of a choline monooxygenase cDNA clone from Amaranthus tricolor and its expressions under stress conditions.";
Cell Res. 11:187-193(2001).
-i- FUNCTION: Catalyzes the first step of the osmoprotectant glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Choline + 2 reduced ferredoxin + O(2)
betaine aldehyde + 2 oxidized ferredoxin + H(2)O.
-!- COFACTOR: Magnesium. Probably binds a 2Fe-2S group and an atom (By similarity).
-!- SIBCELLULAR LOCATION: Chloroplast strong (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast strong (By similarity).
                                  Pfam; PF00355; Rieske; 1.
Monooxygenase; Oxidoreductase; Chloroplast; Iron-sulfur;
Magnesium; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               betaine synthesis.
-!- CATALYTIC ACTIVITY: Choline +
betaine aldehyde + 2 oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core ecaryophyllidae; Caryophyllales; Amaranthaceae; Amaran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update) Choline monooxygenase, chloroplast precursor (EC
                                                                                                                                  EMBL; AF290974; AAK82768.1; -. InterPro; IPR001281; Rieske.
                                                                                                                                                                                                                                                                     entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: By salt, drought and heat stress.
SIMILARITY: BELONGS TO THE CHOLINE MONOOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTLGPAGF 357
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Transit peptide.
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
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CHLOROPLAST (BY SIMILARITY).
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                                                                                                                              GQGKVHAFHNVCTHRA-SILACGTGKKSCFVCPYHGWVFGLDGSLMKATKTEN---QVFD
                                                                                                                                            NDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLN
                                                                                                                                                                        AEDGFTPPSTWYTDPSLYSHELDRIFSKGWQVAGYSDQIKEPNQYFTGSLGNVEYLVCRD 153
                                                                                                                                                                                              SESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQ
                                           IN-RSEFPMESNWKVFCDNYLDSAYHVPYAH 295
                                                               VGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                                                         KKCLGLKEVARVESFHGFIYGCFDQEAPP----LMDYLGDAAWYLEPMFKHS--GGLEL
                                                                                     PKELGLVTL-KVAIWGPFVLISLDRSGSEGTEDVGKEWIGSCA---EEVKKHAFDPSLQF
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IRON-SULFUR (2FE-2S)
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Pred. No. 2.1e-11;
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; C7520F16EAA67A0E CRC64;
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OM protein - protein search, using sw model
                                                      Run on:
January 27, 2003, 08:55:37; Search time 13.1667 Seconds (without alignments) 3278.305 Million cell updates/sec
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Title: Perfect score: Sequence:

US-09-843-250-35
2408
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7 774 32 7 774 32 8 737 30 9 737 30 10 737 30 11 725.5 3 11 725.5 3 12 652.5 27 13 650.5 27	l s c
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naphthalene dloxyg terminal oxygenase biphenyl dioxygena biphenyl dioxygena biphenyl dioxygena biphenyl dioxygena aromatic oxygenase	Description naphthalene dioxyg naphthalene 1,2-di naphthalene 1,2-di polycyclic aromati

45	44	43	42	41	40	39	38	37	36	ω G	34	33	32	31	30
186	214.5	223	224	233.5	251	251	251	254.5	266	271.5	283	287	294	311.5	311.5
7.7	8.9	9.3	9.3	9.7	10.4	10.4	10.4	10.6	11.0	11.3	11.8	11.9	12.2	12.9	12.9
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choline monooxygen	2-nitrotoluene dio	choline monooxygen	choline monooxygen	probable dioxygena	probable choline m	probable choline m	probable choline m	probable dioxygena	biphenyl dioxygena	Rieske 2Fe-2S fami	benzoate 1,2-dioxy	probable aromatic-	probable ring hydr	ring hydroxylating	hypothetical prote

ALIGNMENTS

QУ	Qy Db	Оу	Qy Db	Qy Db	Qу	Qу	Que Bes Mat	A; Ger C; Sul C; Key F; 71 F; 81	A; Mo. A; Res A; Cro C; Cor	R;Ku Gene A;Ti A;Re	RESULT 1 JS0071 naphthal C; Specie C; Date: C; Access
361	301	241 241	181 181	121 121	61	р р	Query Match Best Local : Matches 44:	A; Gene: ndoB C; Superfamil C; Keywords: F; 71-119/Dom F; 81, 83, 101,	A; Molecule A; Residues: A; Cross-ref C; Comment: C; Genetics:	rkela 73, tle: (feren	LT 1 71 thales cies te: 3
DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDYYGDAYYPGVVGKSAIGETSYRGFYRAY 420	FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES 360	QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 	ELVGPPGKVVIKANWKAPAENEVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 	KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 	IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 	MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60 	Query Match 99.8%; Score 2404; DB 2; Length 449; Best Local Similarity 99.8%; Pred. No. 1.2e-183; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	A;Gene: ndoB C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Supwords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein E;71-119/Domain: Rieske [2Fe-2S] homology <rsk>F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status</rsk>	A;Molecule type: DNA A;Residues: 1-449 <kur> A;Residues: 1-449 <kur> A;Residues: 1-449 <kur> C;Comment: Naphthalene dioxydenase system is composed of three proteins. C;Coment: Naphthalene dioxydenase system is composed of three proteins.</kur></kur></kur>	R;Kurkela, S.; Lehvaeslaiho, H.; Palva, E.T.; Teeri, T.H. Gene 73, 355-362, 1988 A;Title: Cloning, nucleotide sequence and characterization of genes encoding naphthal A;Reference number: JS0070; MUID:89211973; PMID:3243438 A;Accession: JS0071	RESULT 1 JS0071 JS0071 naphthalene dioxygenase (EC 1.14.12) ndoB protein - Pseudomonas putida C;Species: Pseudomonas putida C;Species: Pseudomonas putida C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999 C;Accession: JS0071

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Pseudomonas

putida

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Gaps

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(covalent) #status

iron-sulfu

Rieske

enzyme

20-Aug-1999

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R;Denome, S.A.; Young, K.D.

R;Denome, S.A.; Young, K.D.

A;Bescription: Cloning and molecular characterization of genes involved in metabolis A;Bescription: S27631

A;Bescription: S27632

A;Bescription: S27632

A;Accession: S27632

A;Accession: S27632

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-462 < DEN>

A;Cross-references: EMBL:M60405

R;Denome, S.A.; Stanley, D.C.; Olson, E.S.; Young, K.D.

J. Bacteriol. 175, 6890-6901, 1993

A;Title: Metabolism of dibenzothiophene and naphthalene in Pseudomonas strains: comp.

A;Reference number: A49343; MUID:94042852; pMID:8226631

A;Accession: 14-462 < DEE>

A;Cross-references: GB:M60405; NID:9151195; PIDN:AAA16125.1; PID:g294351

A;Accessidues: 14-462 < DEE>

A;Cross-references: GB:M60405; NID:g151195; PIDN:AAA16125.1; PID:g294351

A;Experimental source: strain C18

C:Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske

C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein

F;94,96,114,117/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #statu:
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C;Species: Pseudomonas sp.
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: $27632; Bs9343
C;Accession: $27632; Bs9343
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                                                                                                                                       DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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A:Reference number: A55217; MUID:94209249; PM
A:Accession: C55217
A:Status: preliminary
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                                                                   R; Takizawa, N.; Kaida, N.; Torigoe, J. Bacteriol. 176, 2444-2449, 1994 A; Title: Identification and charact
                                                                                                                               C;Date: 05-May-1995 #sequence_revision
C;Accession: C55217
                                                                                                                                                                    polycyclic aromatic hydrocarbon dioxygenase
C;Species: Pseudomonas putida
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A; Residues: 1-449 <SIM>
A; Cross-references: GB:
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R; Simon, M.J; Osslund, T.D.;
Gene 127, 31-37, 1993
A; Title: Sequences of genes en
A; Reference number: JN0640; MU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFASLAGNAVLPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:M83949; NID:g151384; PIDN:AAA25902.1; PID:g151387 tein is a member of naphthalene dioxygenase multicomponent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.4%;
96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding naphthalene dioxygenase MUID:93252277; PMID:8486285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saunders, R.; Ensley, B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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bred. No. 4.8e-179;
bress 5;
                                                                                                           s:
                                                                                                                                                05-May-1995
                                                                                                                                                                                                                                                                                                                       449
                                                                                                             Moritani,
                                                   on of genes encoding PMID:8157615
                                                                                                                                                                                      (EC 1.14.12.-) iron-sulfur
                                                                                                             Τ.,
                                                                                                             Sawada,
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т.;

Satoh,

S.; Kiyohara aromatic

protein

420

360 360 300 300 240

420

240 180 180

polycyclic

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A;Molecule type: DNA
A;Residues: 1-449 <TRK>
A;Residues: 1-449 <TRK>
A;Residues: 1-449 <TRK>
A;Residues: 1-449 <TRK>
A;Cross-references: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [2FC;Keywords: 2Fe-25; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;71-119/Domain: Rieske [2Fe-25] homology <RSK>
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p:
                                                                                                                a a C
                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-447 <PAR>
A; Cross-references: GB:U49504; NID:g1773273;
A; Experimental source: strain JS42
C; Comment: This enzyme catalyzes the addition
                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: 2-nitrotoluence iron-sulfur protein alpha chain C;Species: Pseudomonas sp.
C;Date: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Au C;Accession: JC5352
R;Parales, J.V.; Kumar, A.; Parales, R.E.; Gibson, D.T. Gene 181, 57-61, 1996
A;Title: Cloning and sequencing of the genes encoding 2-nitrotoluene A;Reference number: JC5350; MUID:97128768; PMID:8973308
A;Accession: JC5352
                                                                                                                                                      C;Superfamily: toluene dioxygenase terminal oxygenase component large (C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur
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     Query Match
Best Local S
Matches 376
                                                                                                ;Keywords: 2Fe-2S; metalloprotein; oxidoreductase;;69-117/Domain: Rieske [2Fe-2S] homology <RSK>;79,81,99,102/Binding site: 2Fe-2S cluster (Cys, H:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Alternate names: 2-nitrotoluence iron-sulfur protein alpha chain;Species: Pseudomonas sp.
;Spate: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Aug-1999
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tive 13; Mismatches 12;
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                   QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                               FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
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QAHISSSNWAEFENASRNWHTELTKTTDR
                                                                              DDNENMETLSQNAKKYQSSNSDQIASLGFGKDVYGDECYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                              FPNNSFLTGSATFKVWNPIDENTTEVWTYAFVEKDMPEDLKRRLADAAQRSIGPAGFWES
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naphthalene dioxygenase (EC 1.14.12.-) large chain - C;Species: Sphingomonas aromaticivorans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #t C;Accession: T31134 C;Accession: T31134 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston A;Genome: plasmid pNL1 c;Superfamily: toluene dioxygenase terminal oxygenase component large chain; C;Keywords: 2Fe-25; metalloprotein; oxidoreductase; Rieske iron-sulfur protein; F;80,82,100,103/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) A; Gene: bphAlf A;Cross-references: C;Genetics: A; Molecule type: DNA A; Residues: 1-459 < ROM> A; Status: preliminary; A; Reference number: A; Accession: T31134 A; Description: Complete sequence A; Reference number: 220992 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Submitted to the EMBL Data Library, July 1998 A;Description: Complete sequence of a 184 kb of the complete sequence Query Match Best Local Matches al Similarity 192; Conserv Conservative EMBL:AF079317; NID:g3378261; PID:g3378275; PIDN:AAD03858 translated 39.7%; 43.9%; 71; Score 957; DB Pred. No. 2.5e-71; Mismatches from GB/EMBL/DDBC catabolic Thurston, DB 2; 162; #text_change 19-May-2000 Length 459; Sphingomonas aromaticivorans plasmid S.J.; Indels Sisk, from 12; E.C.; Sphingomonas Gaps protein #status Rieske 7; arom G pla Σ

128 127 187

GKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAA-LPPEGAGLQMTSK

185 245

LNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK-HSGGLELVGPP 186

LDKSKLGLAPI-RVETYKGFIFGCHDPEAPSLEDYLGDFCWYLDTIWDGPDGGLELLGPP

68

7 8

66

RQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGES

RQPDGSLKAFINSCTHRGNQICHADSGSAKAFVCNYHGWVFGQDGSLVDVPMEERCYHSD 126

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417

YRAYQAHVSSSNWAE 431

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RESULT 7

T31256

terminal oxygenase component large chain homolog - Sphingomonas aromaticivorans posterminal oxygenase component large chain homolog - Sphingomonas aromaticivorans c; Species: Sphingomonas aromaticivorans posterial component large revision 11-Jan-2000 #text_change 19-May-2000 c; Accession: T31256

R; Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, General component complete sequence of a 184 kb catabolic plasmid from Sphingomonas and A. Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas and A. Pescription: T31256

A; Accession: T31256

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-450 <ROM>
A; Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378397; PIDN:AAD03980.1

C; Genetics:
A; Genome: plasmid pNL1
A; Note: bphAla

C; Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieslesse component larg
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LFDNDDGDNLTACTEQSRGWRTAQMDVYTNMALGRSGKREG-FPGDIAAGLVSEHNQRYF
                                                  FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGF
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A:Molecule type: DNA
A;Residues: 1-19, A', 21-383, ATAPATANCVWKW', 397-398, 451, 'R', 453, 'SAATTAFLALLTISFQKLPL
A;Residues: 1-19, CA', 21-383, 'ATAPATANCVWKW', 397-398, 451, 'R', 453, 'SAATTAFLALLTISFQKLPL
A;Cross-references: EMBL:Z37966; NID:g550595; PIDN:CAA86018.1; PID:g550596
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;75-123/Domain: Rieske [2Fe-2S] homology <RSK>
F;85,87,105,108/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
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A;Description: Cloning and sequencing of an E. coli gene homologous
A;Reference number: S49292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: A65031
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
C;Accession: A65031; S49292
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A; Residues: 1-453 <BLAT>
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A; Title: The complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP
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                                         YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                    AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
                                                                                                                                                                                                             RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTL
                                                                                                                                                                                                                                                                                                                                                                                  AENFVGDAYHVGWTHASSL - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK 453
                                                                                    GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT
                                                                                                                                                                                                                                                      QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----
                                                                                                                                                                                                                                                                                               --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
                                                                                                                                                                                                                                                                                                                                         AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD-----GQTARPVWETAKDALQFG
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Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 737; DB 2; Pred. No. 8.3e-51;
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                                                                                                                                                                                                                                                                                                                                                                                  -RSGESIFSSLAGNAALP--
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                                                                                                                                                                                                                                                      ----AEQRLGEVRALRL
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RESULT

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D91054
biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain C; Species: Escherichia coli
C; Species: Escherichia coli
C; Cate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2001
C; Accession: D91054
R; Hayashi, T; Makino, K; Ohnishi, M; Kurokawa, K; Ishii, K; Yokoyama, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, F gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shiba
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C; Superfamily: toluene dio:
C; Keywords: oxidoreductase
A; Molecule A; Residues:
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                                             A; Status: preliminary
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Pred. No. 8.3e-51
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                                                                                                                                                                 u, B.; Glası
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A;Cross-references: GB:AE005174; NID:g12516944; PIDN:AAG57651.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: hcaA1 C;Superfamily: toluene dioxygenase terminal oxygenase component C;Keywords: oxidoreductase
                                                                                                                                                                                          RESULT 11
T31258
                                   R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas A;Reference number: Z20992
                                                                                                                                                   aromatic oxygenase large chain - Sphingomonas aromaticivorans plasmid C; Species: Sphingomonas aromaticivorans
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A; Status: preliminary; translated
                   A; Reference number: A; Accession: T31258
                                                                                                             C; Date: 11-Jan-2000
C; Accession: T31258
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                                                                                                                               11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                      YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK
                                                                                                                                                                                                                                                                                                                                                                                                                   AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
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                                                                                                                                                                                                                                                                  ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
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A;Molecule type: DNA
A;Residues: 1-455 <ROM>
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378399; PIDN:AAD03982.
A;Genetics:
A;Genome: plasmid pNL1
A;Note: bphAlb
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; C;Keywords: 2Fe-25; metalloprotein; Rieske iron-sulfur protein
C;Keywords: 2Fe-25; metalloprotein; Rieske iron-sulfur protein
C;Keywords: 2Fe-25; metalloprotein; Rieske iron-sulfur protein
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                      NYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGI
  DYSRYMDLKEGWLDRR--IFSDADIYEEELYRIFARSWLFVAHESQIPSSGDFLTTHMGE
                                                                                    Conservative
                                                                                                   30.1%;
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                                                                                  Score 725.5; DB 2;
Pred. No. 6.9e-50;
13; Mismatches 169;
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A; Residues: 1-450 <TAN>
A; Cross-references: GB:L04642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           benzene 1,2-dioxygenase (EC 1.14.12.3) terminal oxygenase component large chain C;Species: Pseudomonas putida C;Date: 19-May-1994 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000 C;Accession: JN0812 R;Tan, H.M.; Tang, H.Y.; Joannou, C.L.; Abdel-Wahab, N.H.; Mason, J.R. Gene 130, 33-39, 1993 Gene 130, 33-39, 1993 A;Title: The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenas A;Reference number: JN0810; MUID:93345820; PMID:8344526 A;Accession: JN0812
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                                     PLKARVETYKGLIFANWDENAIDLDTYLGEAKFYMDHMLDRTEAGTEVIPGIQKWVIPCN
                                                                                                           QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA----
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                                     368
                                                                                                                                                                                                                                                                                                                          138 --VARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
   EIQHILRGHKARSRPFNAEMSMDQTVDNDPVYPGRISNNVYSEEAARGLYAHWLRMMTSP
                                   TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS 427
                                                                      PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
                                                                                           TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWESDDNDNME
                                                                                                                                             GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
                                                                                                                                                                              VLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                                  WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                                                                                                                                                                                                                                     WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                                                                                                               QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA----
                                                                                                                                                                                                                                                                                                                                                                                               VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                  IYTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMMTSPDW
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-CLNKKEWS

148

251

94

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RESULT 13
A36516
A36516
Coluene dioxygenase (EC 1.14.12.11) terminal oxygenase component large chain Coluene dioxygenase putida
Coluene i 15-Feb-1991 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
                                                                                         C;Superfamily: toluene dioxygenase terminal oxygenase component large chain: C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidorec F;86-134/Domain: Rieske [2Fe-2S] homology <RSK> F;96-98,116,119/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 264, 14940-14946, 1989
A:Title: Toluene degradation by Pseudomonas
A:Reference number: A36516; MUID:89359301;
                                                                                                                                                                                                                                             A; Cross-references: GB:J04996; NID:g151600; A; Experimental source: strain F1
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-450 <ZYL>
                                                                                                                                                                                                                                        A; Experimental source: strain
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                           Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb"PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWESD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP----
    Conservative
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                           27.0%;
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71;
                           Score 650.5; DB 1; Pred. No. 6.4e-44;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                             putida F1. pmID:2670929
                                                                                                                                                                                                                                                                 PIDN: AAA26005.1;
  181;
                                            Length 450;
    Indels
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    25;
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  Gaps
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RESULT 14

$51757

biphenyl dioxygenase (EC 1.14.-.-) large chain - Rhodococcus globerulus
C;Species: Rhodococcus globerulus
C;Species: Rhodococcus globerulus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: $51757
R;Asturias; J.A.; Diaz, E.; Timmis, K.N.
submitted to the EMBL Data Library, July 1994
A;Description: Evolutionary relationship of the biphenyl dioxygenase of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: bphAl
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; R:
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;89-137/Domain: Rieske [2Fe-2S] homology <RSK>
F;99,101,119,122/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
biphenyl dioxygenase (EC 1.14.12.-) terminal oxygenase component C; Species: Pseudomonas sp. C; Date: 04-Mar-1993 #sequence_revision 06-Jan-1995 #text_change 0 C; Accession: B41858 R; Erickson, B.D.; Mondello, F.J. J. Bacteriol. 174, 2903-2912, 1992 A; Title: Nucleotide sequencing and transcriptional mapping of the
                                                                                                                                                  RESULT
B41858
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A; Cross-references: EMBL: X80041;
A; Cross-references: Experimental source: strain P6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QCRHRGMRICRADGGNAKSFTCSYHGWAYDSAGNLVSVPFQQEAFPD-LKKEDWGPLK-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLG-LKEV 138
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                                                                                                                                                                                                                                                                                                                   WVEIQSVLRGHKARSRPFNAEMSLRETNTADPDWPGTI-SYVYSEEAARGFYAHWSRMMT
                                                                                                                                                                                                                                                                                                                                                          METASQNGKKYQSRDSDLLSNLGFGEDYYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVS 425
                                                                                                                                                                                                                                                                                                                                                                                                   FLPGINTIRTWHPRGPHEIEVWSFTVVDADAPAEIKEEYRRQTIRTFSAGGVFDQDDGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHGSGFYIGEMGTLAAVMGMKILEYYTSGPAAEKAAKRLGSAVRGSQATGQHMTVFPTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGMGVLWDGYSGVHSADLVPELMAF--GGAKQERLNKEIGDVRARIYRSHLNCTVFPNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYTDEALYQQELELIFGRSWLLLGHETQIPKAGDFMTQYMGEDPVIVSRQRDGSISVFLN 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148;
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33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 639; DB 2; I
Pred. No. 5.5e-43;
4; Mismatches 187;
    transcriptional mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biphenyl dioxygenase of the gram-positve
                                                                                   #text_change 05-May-2000
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                                                                                                                            large chain
    genes encoding bipheny
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                                                                                                                               Pseudomo
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Search

time: 14.1667 secs

completed: January 27, 2003, 09:03:49

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A;Gene: bphAl; bphA (;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske (C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske (C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidoreductase; E;90-138/Domain: Rieske (2Fe-2S] homology <RSK> F;100,102,120,123/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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A; Residues: 1-459 <ERI>
A; Cross-references: GB: M86348; NID: g349602;
A; Experimental source: strain LB400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A41858; A; Accession: B41858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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les 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     KCLGLKEV-----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                                                                                                                 VR-RMVGQHM--TIFPTCSFLPTFNNIRIWHPRGPNEIEVWAFTLVDADAPAEIKEEYRR 372
                                                                                                                                                                                                                                                QIPTK-GNQFRAAWGGHGSGWYVDEPGSLLAVMGPKVTQYWTEGPAAELAEQRLGHTGMP
                                                                                                                                                                                                                                                                                         QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAK-----
                                                                                                                                                                                                                                                                                                                                                                         GPPGKVVIKANWKAPAENFVGDAYHVG-WTHASSLRSGESIFSSLAGNAALPPEG--AGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
VYAEEAARGMYHHWMRMMSEPSWA
                                      AIGETSYRGFYRAYQAHVSSSNWA 430
                                                                                 HNIRNFSAGGVFEQDDGENWVEIQKGLRGYKAKSQPLNAQMGLGRSQTGHPDFPGNVG-Y
                                                                                                                        SVQRTLGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKS
                                                                                                                                                                                                       VRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLAD
                                                                                                                                                                                                                                                                                                                                  GGMQKWVIPCNWKFAAEQFCSDMYHAGTTTHLSGILAG---
                                                                                                                                                                                                                                                                                                                                                                                                               DC-GFDKAEWGPLQARVATYKGLVFANWDVQAPDLETYLGDARPYMDVMLDRTPAGTVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKSTKVFLNQCRHRGMRICRSDAGNAKAFTCSYHGWAYDIAGKLVNVPFEKEAFCDKKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKGLLDPR-IYADQSLYELELERVFGRSWLLLGHESHVPETGDFLATYMGEDPVVMVRQK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUID:92234948; PMID:1569021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 617.5; DB
Pred. No. 2.8e-41
9; Mismatches 18
  455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:AAB63425.1; PID:g151084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                         -QERLNKEIGD
                                                                                                                                                                                                                                                                                                                                  -IPPEMDLSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                          346
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Run on: OM protein - protein search, using sw model January 27, 2003, 08:46:47; Search time 29.1667 Seconds (without alignments) 2051.298 Million cell updates/sec GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

Perfect score: Title: US-09-843-250-35 2408

Scoring table: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR

Total number of hits satisfying chosen parameters:

908470

908470 seqs, 133250620 residues

Searched:

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_101002:*

1: /SIDS2/gcgdata/g
2: /SIDS2/gcgdata/g
3: /SIDS2/gcgdata/g
4: /SIDS2/gcgdata/g
4: /SIDS2/gcgdata/g
5: /SIDS2/gcgdata/g
6: /SIDS2/gcgdata/g
6: /SIDS2/gcgdata/g
9: /SIDS2/gcgdata/g
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10: /SIDS2/gcgdata/
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14: /SIDS2/gcgdata/
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16: /SIDS2/gcgdata/
16: /SIDS2/gcgdata/
17: /SIDS2/gcgdata/
16: /SIDS2/gcgdata/
17: /SIDS2/gcgdata/ 18: 19: 20: 21: 22: 23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: * /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	AAB12568	21		99.7	2400	10
	AAB12583	21		99.8	2402	9
Naphthalene dioxyg	AAB12580	21	449	99.8	2403	80
	AAB12579	21		99.8	2403	7
	AAB12577	21		99.8	2404	0
	AAB12567	21		99.9	2405	Ų
	AAB12566	21		99.9	2405	4
	AAB12565	21		99.9	2405	ω
	AAB12582	21		99.9	2406	2
Naphthalene dioxyg	AAB12581	21		100.0	2408	1
Description	ID	DB	Length	Query	Score	Result No.

ALIGNMENTS

RESULT 1 AAB12581	LT 1 2581	
Ħ	AAB12581 sta	AAB12581 standard; Protein; 449 AA.
XX		
AC	AAB12581;	
XX		
DΤ	09-NOV-2000	09-NOV-2000 (first entry)
XX		
DE	Naphthalene	Naphthalene dioxygenase mutant F352L protein sequence SEQ ID NO:35.
XX		•
ΚW	Pseudomonas	Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO;

rseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral diol; polymer; resin; pharmaceutical; rubber industry; bioremediation.

Pseudomonas sp. Synthetic.

29-JUN-2000 WO200037480-A1

26-OCT-1999; 99WO-US25079

VALUE OF STREET 26-OCT-1998; 98US-0105575

(IOWA) UNIV IOWA RES FOUND.

Parales R, Gibson D, Resnick Ś Lee Χ,

N-PSDB; AAA65355 WPI; 2000-452174/39.

Novel naphthalene dioxygenase mutant having a specific amino acid

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Best Local 9
    AAB12582 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydroanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (')-(15,2R)-cls-napththalene dihydrodiol, (- or +)-cls-biphenyl-3,4-dihydrodiol, (18,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an
                                                                                                            421
                                                                                                                                                   421
                                                                                                                                                                                               361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG 60
                                                                                                                             QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                          DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                             FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
                                                                                                                                                                                                                                                                                                                  FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
                                                                                                                                                                                                                                                                                                                                                             QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                           ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 131-133; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
    Protein; 449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2408; DB 21;
Pred. No. 1.6e-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                              involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, caenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, caenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, caenaphthylene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene accorresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represents
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related complex (I) comprising several polypeptides which contain a alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 133-134; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200037480-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Naphthalene dioxygenase mutant F352I protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducible multi-component enzyme; alpha subunit;
121 KDLYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                          61
                                                                                61
                                                                                                                    1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                          1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes a naphthalene dioxygenase (NDO)
                                                                IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                          IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                  448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-452174/39.
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R, Gibson D,
                                                                                                                                                                                                                                                                                449 AA;
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain NCIB 9816-4; naphthalene dioxygenase;
                                                                                                                                                                                                                  99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Resnick
                                                                                                                                                                                                  1;
                                                                                                                                                                                                                  Score 2406; DB 21;
Pred. No. 2.5e-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ß
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                  0;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                    Length 449;
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bioremediation
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The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (')-(1S,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which
                                                                                                                                                                                                                  Novel naphthalene dioxygenase mutant having a specific amino substitution for preparing chiral diols for use in the polyme pharmaceutical or rubber industry and for carrying out bioren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDc inducible multi-component enzyme; alpha subunit; mutant; chiral polymer; resin; pharmaceutical; rubber industry; bioremediation
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26-OCT-1999; 29-JUN-2000

99WO-US25079

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (I) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with phenanthrene, 1,2-dihydroxy-1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxphenanthrene which CC involves contacting them with phenanthrene. The polypeptides and the CC involves contacting them with phenanthrene. The polypeptides and the CC involves contacting them with phenanthrene. The polypeptides and the CC involves contacting them with phenanthrene. The polypeptides and the CC involves contacting them with phenanthrene. The polypeptides and the CC involves contacting them with penanthrene. The polypeptides and the CC careainthiphene, naphthalene, anthracene, phenanthrene, dibenzo(1,4)dioxan, CC caenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, CC caenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, CC cells are useful for preparing chiral diols for use in the polymer, CC cells are useful for preparing chiral diols for use in the polymer, CC anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC camplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 99-100; 151pp; English
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                                      DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                   ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                              IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                      FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
                                                                                                                                                             QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                  QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                            KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                             IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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bioremediation
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RESULT 5
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related complex (I) comprising several polypeptides which contain an calpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(Is,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-ci dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydromaphthalene, which involves contacting them with naphthalene polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy
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                                            acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroganthracen, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDO related complex alpha subunit protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB12567 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a naphthalene dioxygenase (NDO) or NDO
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AA;
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bioremediation.
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bioremediation
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Matches 448; Best Local Similarity

Conservative

99.98;

Score 2405; DB 21; Pred. No. 3.1e-223;

Length 449;

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Gaps

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Query Match

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RESULT 6
AAB12577
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                                                          Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                          Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral compolymer; resin; pharmaceutical; rubber industry; bioremediation.
                       Disclosure;
                                                                                                                                                         Parales
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                                                                                                                                                                                                                                                                                                                   Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                              Naphthalene dioxygenase alpha subunit protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12577 standard; Protein;
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                      Page 118-120; 151pp;
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The

present

invention

describes a naphthalene dioxygenase (NDO) or NDO

RESULT 7
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ID AAB1
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AC AAB1
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standard; Protein; 449

Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; inducible multi-component enzyme; alpha subunit; mutant; chi

Naphthalene dioxygenase mutant F352A protein sequence

SEQ ID

NO:33.

chiral diol;

(first entry)

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Best Local
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QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                    DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                               ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
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                                                                ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
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                                                                                                                                      dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxphenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
                  aromatic compound such as indene, 1.2-dhlydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydronanthracene, or 9,10-dihydrophenanthrene a
                                                                                                                                                                                                                                                                                                                                                   alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15.2R)-cis-rapththalene dihydrodiol, (- or +)-cis-biphenyl-3.4-dihydrodiol, (15.2R) cis-phenauthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a naphthalene dioxygenase (NDO) or related complex (I) comprising several polypeptides which contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 129-131; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymer; resin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Naphthalene dioxygenase mutant F352T protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducible multi-component enzyme; alpha subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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dihydro dihydroxy compound. The polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Resnick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant; chiral bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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AC AAB1
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DT 09-1
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                                                                                                                                                                                                               Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                             AAB12583 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                  Parales
                                             (IOWA ) UNIV IOWA RES
                                                                                                          26-OCT-1999;
                                                                                                                                                                                                                                          polymer; resin;
                                                                                                                                                                                                                                                                     Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO;
                                                                            26-0CT-1998;
                                                                                                                                                                                                                                                                                                  Naphthalene dioxygenase mutant F352W protein sequence SEQ ID NO:58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                        .nducible multi-component enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                 ₽,
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                 Gibson
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                           98US-0105575
                                                                                                          99WO-US25079
                                                                                                                                                                                                                                          pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                              FOUND
                  Resnick
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Pred. No. 4.9e-223;
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                                                                                                                                                                                                                                        rubber industry; bioremediation
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                                                                                                                                                                                                                                                     alpha subunit; mutant; chiral diol;
               Lee
               Χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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NPSDB; AAA65376.

Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation pharmaceutical or rubber industry and for carrying out bioremediation pharmaceutical or rubber industry and for carrying out bioremediation related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(18, 2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (18, 2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, and 1,2-dihydronaphthalene, phenanthrene or 3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihy
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                   QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                     FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                            DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTWGPAGFWES
                                                                                                                                                                                                                           QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                               QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                          ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                   KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                      ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                               KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%;
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Pred. No. 6.1e-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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CC Fel
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CC Ginv
C
                                                                                    Вb
                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the most cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The presents sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cexamplification of the present invention.
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13;
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                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDO related
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                                                                                                                    1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
                            IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                    MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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)B; AAA65342.
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                                                                                                                                                                                                                                                                                                                                    449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (I) comprising several
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ď
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99.6%;
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                                                                                                                                                                                                                                           Score 2400; DB 21; Pred. No. 9.5e-223;
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veral polypeptides which contain an
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                                                                                                                                                                                                                                                                           449;
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RESULT 11
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                                                                                                                         Novel naphthalene dioxygenase mutant having a specific amino acid
substitution for preparing chiral diols for use in the polymer, r
pharmaceutical or rubber industry and for carrying out bioremedia
                                                                                                                                                                                                          Parales
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                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp. strain NCLB y810-4 inducible multi-component enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB12578 standard;
                                                                                                                                                                                    WPI; 2000-452174/39.
                                                                                                                                                                                                                                (IOWA ) UNIV IOWA
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                                                                                                                                                                                                                                                                                                                                                             Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                   polymer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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                                                                                                                                                                                                         R, Gibson D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                dioxygenase mutant F352G protein sequence SEQ
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                                                                                                                                                                                                                                                        98US-0105575
                                                                                                                                                                                                                                                                                                                                                                                                         strain NCIB 9816-4; naphthalene dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical;
                                                                                                                                                                                                                                 RES
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                                                                                                                                                                                                                                                                                                                                                                                    rubber industry;
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                                                                                                                                                                                                                                                                                                                                                                                              alpha subunit;
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                                                                                                                                                                                                           Lee
                                                                                                                                                                                                                                                                                                                                                                                   mutant; chiral bioremediation.
                                                                                                                           polymer, resin, bioremediation
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related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol,
Claim

9;

Page 126-127; 151pp; English

present invention

describes a naphthalene dioxygenase (NDO)

or NDO

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RESULT 12
AAB12584
ID AAB12
XX Pseud
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KW Polym
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-CC dihydroxy-1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which compound such as indene, 1,2-dihydrophenanthrene which they oxidise an are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, CC benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, CC denaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, CC acenaphthylene, plo-dihydronanthracene, or 9,10-dihydrophenanthrene a CC corresponding dihydro dihydroxy compound. The polypeptides and the host CC cells are useful for preparing chiral diols for use in the polymer, CC resin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 448
                                                                                                             Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d
                                                                                                                                                                     Naphthalene dioxygenase mutant F352Y protein sequence SEQ ID NO:59
                                                                                                                                                                                                             09-NOV-2000
                                                                                                                                                                                                                                                                                       AAB12584 standard; Protein;
                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                     421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
                                                                                                                                                                                                                                                                                                                                                                                   QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                                                                                                                                                                                                                                                                                                                                                                                        QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                             resin;
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                                                                                                                                                                                                           (first entry)
                                                                                             pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2400; DB 21;
Pred. No. 9.5e-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                           industry;
                                                                                           mutant; chiral
bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 449;
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                                                                                                           chiral diol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Qγ

KDLYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL

KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE

ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL

240 180

240

181 121 121 61 61

Вb Qy DЪ Qγ

1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG

Conservative

0;

Mismatches

Indels

0;

Gaps

0,

60

60

IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG

Qy В δÃ В Qγ Вb

301 301

FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTYGPAGFWES FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV

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dihydroxyindan, 1,2'dihydroxy-1,2,3,4-tetrahydronaphthalene, which convolves contacting them with naphthalene, biphenyl, phenanthrene, involves contacting them with naphthalene respectively. The polypeptides and convolves contacting them with phenanthrene. The polypeptides and convolves contacting them with phenanthrene. The polypeptides and the lost cells are also used in bioremediation in which they oxidise an convolves contacting them with phenanthrene. The polypeptides and the lost cells are also used in bioremediation in which they oxidise an convolve contacting them with phenanthrene. The polypeptides and the lost cells are also used in bioremediation in which they oxidise an convolve compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzofuran, convolve corresponding dihydro dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host colls are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the covve
Best Local Similarity Matches 447; Conserv
                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a naphthalene dioxygenase (NDO) or NI related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted anino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(1S,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,2-dihydr
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 144-145; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1998;
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DB; AAA65377.
                                                                                                                                                                      448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibson D,
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                                             99.6%;
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                                         Score 2398;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s
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                                     1.5e-222;
                                                                                       DB 21;
                                                                           Length 448;
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Query Match

Length 449;

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RESULT 13
AAB12569
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Qy
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                      involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1.4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the
                                                                                                                                                                                                                     involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,3-dihydrophenanthrene which
                                                                                                                                                                                                                                                                                                                                                     related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremediate
            exemplification of
                                                                                                                                                                                                                                                                                                 (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxylndan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a naphthalene dioxygenase (NDO) or NDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 104-105; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA65343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson D,
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        the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymer, resin, bioremediation
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                              represents
the
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equence

449

A A

polymer, resin bioremediation

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RESULT 14
AAB12570
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Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bioremedia.
                                                                                                                                                                                   26-OCT-1999;
                                                                                                                                                                                                               29-JUN-2000
                                                                                                                                                                                                                                                                                                             Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d polymer; resin; pharmaceutical; rubber industry; bioremediation.
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                                                                                                   Parales
                                                                                                                            (IOWA ) UNIV IOWA RES
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                                                                                                 R, Gibson D,
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                                                                                                                                                                                                                                                                                                                                                                       complex alpha subunit protein sequence
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                                                                                                   Resnick
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Pred. No. 2.9e-222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc related complex (1) comprising several polypeptides which contain an collapse subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing cc (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-cc dihydrodylol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-cc dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which cc involves contacting them with naphthalene, biphenyl, phenanthrene, cl indene, and 1,2-dihydroxphenanthrene polypeptides and cc the host cells are also useful for preparing 1,2-dihydroxy-1,2-cc dihydroxy-1,2-cc dihydroxy-1,2-cc dihydroxy-1,2-cc dihydroxy-1,2-cc dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-cc dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-cc dihydroxy-1,2-cc useful compound such as indene, 1,2-dihydroxphenanthrene, cc benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, cc benzocyclohelpt-1-ene, anthracene, biphenyl, fluorene, dibenzofuran, cc dibenzothiophene, 9,1-dihydroxanthracene, or 9,10-dihydroxphenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cc lis are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, compounds useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer.
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09-NOV-2000
                                                                                             AAB12571 standard; Protein; 449 AA
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                                                                                                                                                                                                                                                                                                                 DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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Pred. No. 1.
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CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydroxphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydromaphthalene respectively. The polypeptides and CC indene, and 1,2-dihydromaphthalene respectively. The polypeptides and CC involves contacting them with phenanthrene. 1,2-dihydroxy-1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which CC involves contacting them with phenanthrene. The polypeptides and the CC host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, CC benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, CC accamaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, CC dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host CC cells are useful for preparing chiral diols for use in the polymer, CC resin, pharmaceutical or rubber industry. The present sequence represents an aphthalene dioxygenase (NDO) mutant alpha subunit, given in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related complex (I) comprising several polypeptides which contains substituted amino acids at specific alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 107-109; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
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N-PSDB; AAA65345.
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                                IDEVIVSRONDGSIKAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                        MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                          MNYKNKILVSESGLTQKHLIHGDEELFQHELRTIXARNWLFLTHDSLIPSPGDYVTAKMG
IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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Pred. No. 6.3e
13; Mismatches
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Search completed: January 27, 2003, 08:58:51 Job time : 30.1667 secs	QAHVSSSNWAEFEDASSTWHTELTKTTDR 449	QAHVSSSNWAEFEHASSTWHTELTKTTDR 449	DDNDNMETASQNGKKYQSRDSDLISNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	DDNDNMETASQNGKKYQSRDSDLLSNLGEGEDVYGDAVYPGVVGKSAIGETSYRGEYRAY 420	FPNNSVLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADAVQRTVGPAGFWES 360	FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES 360	QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVPARIYRSHLNCTV 300	QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300	ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRTGESIFSSLAGNAVLPPEGAGL 240	ELVGPPGKVVIKANWKAPAENFYGDAYHYGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240	KELYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPSLMDYLGDAAWYLEPIFKHSGGL 180	KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180

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Result
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Maximum DB
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Match
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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US-09-776-490-19
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US-08-96-063C-4
US-08-976-063C-4
US-09-776-491-12
US-09-776-491-12
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US-09-776-490-15
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US-09-776-490-15
US-09-776-491-13
US-09-776-491-15
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Sequence 10253, A
Sequence 6140, Ap
Sequence 11692, Ap
Sequence 19, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 15, Appl
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	TING DATE: 2000-03-21 PPILCATION NUMBER: 60/206,84 TLING DATE: 2000-05-23 PPLICATION NUMBER: 60/207,72 PPLICATION NUMBER: 60/242,57 PPLICATION NUMBER: 60/242,57 TLING DATE: 2000-10-23 PPLICATION NUMBER: 60/253,62 PPLICATION NUMBER: 60/257,93 PPLICATION NUMBER: 60/257,93 PPLICATION NUMBER: 60/257,93 PPLICATION NUMBER: 60/269,30 PRECIATION NUMBER: 60/269,30	RESULT 1 US-09-815-242-10253 ; Sequence 10253, Application US/09815242 ; Patent No. US20020061569A1 ; GENERAL INFORMATION: APPLICANT: Hoselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Yeselbeck, Tobin D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Yamamoto, Robert T. APPLICANT: Yamamoto, Robert T. APPLICANT: Yu, H. Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Tokaryotes FILE REFERENCE: ELITAR, 011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: US/09/815,242	ALIGNMENTS	24 104 4.3 35 10 US-09-776-490-18 Sequen. 25 104 4.3 35 10 US-09-776-491-11 Sequen. 26 103 4.3 35 10 US-09-776-491-11 Sequen. 27 103 4.3 35 10 US-09-776-491-11 Sequen. 28 102 4.2 35 10 US-09-776-491-8 Sequen. 29 102 4.2 35 10 US-09-776-491-8 Sequen. 30 102 4.2 35 10 US-09-776-491-8 Sequen. 31 102 4.2 35 10 US-09-776-491-8 Sequen. 32 102 4.2 35 10 US-09-776-491-8 Sequen. 33 101.5 4.2 376 9 US-09-712-363-246 Sequen. 34 101 4.2 17 10 US-09-776-490-44 Sequen. 35 101 4.2 17 10 US-09-776-491-45 Sequen. 36 101 4.2 17 10 US-09-776-491-17 Sequen. 37 101 4.2 17 10 US-09-776-491-17 Sequen. 38 100 4.2 35 10 US-09-776-491-17 Sequen. 39 100 4.2 35 10 US-09-776-491-17 Sequen. 40 95 3.9 17 10 US-09-776-491-18 Sequen. 41 95 3.9 920 10 US-09-815-242-12181 Sequen. 42 95 3.9 920 10 US-09-815-242-13148 Sequen. 38 Sequen. 39 Sequen.
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Query Match Best Local Similarity

30.6%;

Score 737; DB 10; Pred. No. 1.3e-57;

Length 453;

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В

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; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6140
                                                                                                                                                                                                                                                                     APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1900-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
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                                                                                                                                                                           PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 6140
TLENGTH: 490
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                                          Best Local Similarity Matches 118; Conserv
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OCHIAI, KEIKO
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TATEISHI, NAOKO
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                                            Conservative
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                                        Score 377; DB 9; I
Pred. No. 1.3e-25;
6; Mismatches 215;
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US-09-815-242-11692
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                               SOFTWARE: FastSEQ
SEQ ID NO 11692
LENGTH: 385
Query Match
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                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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                                                   TYPE: PRT
ORGANISM: Klebsiella
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Zyskind, Judith w.
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Trawick, John D.
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  Score
  376.5;
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US-09-815-242-5097
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                                                                                                                              ; ORGANISM: Pseudomonas aeruginosa 
US-09-815-242-5097
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                                       Query Match
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5097
LENGTH: 424
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Matches 110; Conservative
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
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                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 ---WTHASSL--RSGESIFSSLAGNAALPPEGAGLQMTSKYG--SGMGVLWDGYSGVHSA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 FDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAENFVGDAYHVG 210
  25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 IFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEA 93
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALNPEVRPV-YAHRERLQAEFGERRADQMVNETRNLCLYPNVYLMDQFSTQIRVIRPIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNADVQPLEAYLGETCKIIDLIVDQAPEGLEVLKGSSSYVYEGNWKLGAEN-GADGYHVS
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                                           Conservative
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                                         Score 341.5; I
Pred. No. 1.5e-
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8; Mismatches 154;
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nes 177;
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                                                                                                                       INFORMATION FOR SEQ ID NO: 19:
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                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 28234
COMPUTER READABLE FORM:
MOLECULE TYPE:
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: BELL, SELTZER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Briggs, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWESDDN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VYRNFLFIHYGARQASLETYLGQAKDYIDLICDQSEAELEIIPGGFEHSIKANWKLLAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKC---LGLKEVARV 141
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                                       STRANDEDNESS: <Unknown>
                                                             TYPE:
                                                                                                                                                                                                                              NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943 REFERENCE/DOCKET NUMBER: 57
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
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                                                                                                                                               TELEX:
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                                                                              LENGTH: 35 amino acids
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RESULT 7
US-09-776-490-20
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US-09-776-491-19
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Best Local Similarity
Matches 33; Conserv
Sequence 20, Application US/09776490 Patent No. US20010012886A1
                                                                                                                                                                                        Query Match 7.7%;
Best Local Similarity 94.3%;
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                           TELEX: 575102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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1 NVCRHRGKTLVSVEAGNAKGPVCSYHGWGFGSNGK 35
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                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spruill, W. Murray
REGISTRATION NUMBER: 37,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BELL, S
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
--- CELL DEATH AND DISEASE RESISTANCE IN PLAI
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FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O.
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Johal, Gurmukh S.
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Drawer 34009
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                                                                                                                                                                                      Score 185; DB 10;
Pred. No. 3.1e-10;
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Pred. No. 3.1e-10;
                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                          DB 10;
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                                                                                                                                                                                                        Length 35;
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Matches
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Sequence 20, Application US/09776491 Patent No. US20010013135A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Johal, Gurmukh S.
Gray, John
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                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
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                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                        ADDRESSEE: BELL, SELTZER, PARK & GIBSO
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. US20010013135A1th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001
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                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-881-3175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                   Johal, u. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575102
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85.7%;
                                                                                                                                                                                                                     CELL DEATH AND DISEASE RESISTANCE
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Pred. No. 3e-09;
2; Mismatches
                                                                                                                                                       PARK & GIBSON
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OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

COMPUTER:

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TOPOLOGY: Innear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-776-491-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 20:
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                                                                                                     APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-WAR-1997
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MUTRAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER,
STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Charlotte
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: No. US20010012886A1th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-881-3175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 35 amino acids
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85.7%;
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Pred. No. 3e-09;
2; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-776-491-21
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US-09-776-491-21
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Query Match 7.0%;
Best Local Similarity 80.0%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0 Matches 28; Conservative
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSE: BELL, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 65
                                                                                                                                                                   LENGTH: 35 amino acids
TYPE: amino acid
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STATE: No. US20010013135Alth Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,943
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TELEX: 575102
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                                                                                                                                                                                                                                                                     ELEFAX: 919-881-3175
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80.0%;
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                                                                                                                                                     <Unknown>
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                                   Score 168;
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Pred. No. 1e-08;
                   Pred. No. 1e-08;
Mismatches
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                                                                                                 21:
                                     DB 10; Length 35;
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US-08-976-063C-4
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Baye
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alexander Steinbuchal; Horst Priefert; Jurgen Rabenhorst TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF TITLE OF INVENTION: CONTERNYL ALCOHOL, CONTERNYLALDEHYDE, FERULIC ACTITLE OF INVENTION: ACID AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 196 49 655.1 (Germany)
FILING DATE: 29-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE
STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
   208
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                                    240 L 240
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TYPE: a
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CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                    92
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: HP VECTRA
OPERATING SYSTEM: D
                                                                                                                                                                                                                                                                                                                      34 IFARN--WLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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Н
                                                                     DNLM-DLTHETYVHASSIGQKEIDEAPVSTRVEGDTVITSRYMDNVMAPPFWRAALRGNG 207
                                                                                                        ENFVGDAYHVGWTHASSLR---
                                                                                                                                           ERYGFIWVWPGDRELADPALIHHL---EWADNPEWAYGGGL------YHIACDYRLMI 148
                                                                                                                                                                              SFHGFIY----GCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPA 199
                                                                                                                                                                                                                                                  EAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLG---LKEVARVE 142
                                                                                                                                                                                                                                                                                     MFPKNAWYVACTPDEIADKP---LGRQICNEKIVFYRGPEGRVAAVEDFCPHRGAPL---
                                                                                                                                                                                                                 ----SLGFVRDGKLICGYHGLEMGCEGKTLAMP-------GQRVQGFPCIKSYA-VE 99
   208
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                                                                                                                                                                                                                                                                                                                                                       Score 118.5; DB 1;
Pred. No. 0.0068;
0; Mismatches 78;
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                                                                                                        -SGESIFSS-LAGNAALPP-----EGAG 239
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                                                                                                                                                                                                                                                                                     54
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RESULT 13
US-09-776-491-12
; Sequence 12, Application US/09776491
; Patent No. US200110013135A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
"hes 18; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-776-490-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-76-490-12
; Sequence 12, Application US/09776490
; Patent No. US20010012886A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 575102
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                           1 NOCRHRGMRICRADAGNAKAPTCSYHGWAYDTAG
NUMBER OF SEQUENCES: 65
CORRESONDENCE ADDRESS:
CORRESSE: BELL, SELTZER,
ADDRESSEE: B.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                            APPLICANT: Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Un)
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                     TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/776,490 FILING DATE: 02-Feb-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Dra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-881-3175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                         Johal, Gurmukh S. Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <Unknown>
                                                                                CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 110; DB 10
Pred. No. 0.0014;
                      PARK & GIBSON
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-776-491-12
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US-09-776-490-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.6%;
Best Local Similarity 52.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 575102
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NQCRHRGMRICRADAGNAKAPTCSYHGWAYDTAG 34
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
                                         APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Briggs, Steven P. Johal, Gurmukh S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 28234
                                                                                                                                                                                                                                                                                                        CITY: Charlotte
STATE: No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: No. US20
APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 5718-4
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                                                                                                                                                                                                                                                                                                    US20010012886Alth Carolina
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Pred. No. 0.0014;
4; Mismatches 12;
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-776-490-14
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US-09-776-491-14
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Patent No. US20010013135A1
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal Gurmukh S.
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            INFORMATION FOR SEQ ID NO: 14:
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Local Similarity 52.9%;
es 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/776,491
FILING DATE: 02-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/810,009 FILING DATE: 04-MAR-1997 ATTORNEY/AGENT INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
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                                                                             LENGTH: 35 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                      NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
                                                                                                                                                             TELEFAX: 919-881-3175
TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Charlotte STATE: No. US20010013135Alth Carolina
                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BELL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109; DB 10
Pred. No. 0.0017;
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Osery Part Local Similarity 4.5%; Score 109; DB 10; Length 35; Best Local 13; Conservative 3; W. Fred. No. 0,0017; Indels 0; Gaps 0; Oy 79 NVERBRACTUSVENANKSPYCSYMGARCENSUL 112
Db 1 NOTENBORRICHAGONAKSPYCSYMGAYDSNG 34

Search Compileted: January 27, 2003, 09:20:58

Job time: 8 secs
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1

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Run on:
                                                                                                       OM protein - protein search, using sw model
January 27, 2003, 08:56:07; Search time 10.1667 Seconds (without alignments) 1299.432 Million cell updates/sec
                                                                                                                                                                               GenCore version 5.1.3 Compugen Ltd.
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Title: Perfect score: Sequence: US-09-843-250-36 2408 1 MNYNNKILVSESGL MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result No.
93	94	94	94.5	95	99.5	100	101	101	102	102	103	103.5	103.5	104	106	108	108	108	109	110	112.5	168	174	185	223	224	Score
3.9	. 0	3.9	3.9	3.9	4.1	4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.3	4.3	4.4	4.5	4.5	4.5	4.5	4.6	4.7	7.0	7.2	7.7	9.3	9.3	Query Match Length
35	560	560	350	17	256	35	17	17	35	35	35	649	432	35	35	622	35	ω	35	35	379	35	35	35	439	446	ength DB
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US-08-810-009-16	US-08-812-829-6	US-08-814-052-6	US-08-828-922-1	US-08-810-009-46	US-09-325-932A-57	US-08-810-009-17	US-08-810-009-45	US-08-810-009-44	US-08-810-009-10	US-08-810-009-8	US-08-810-009-11	US-08-809-326A-15	US-08-809-326A-16	US-08-810-009-18	US-08-810-009-9	US-09-311-626B-4	US-08-810-009-15	US-08-810-009-13	US-08-810-009-14	US-08-810-009-12	US-09-028-934-36	US-08-810-009-21	US-08-810-009-20	-810-009-	US-09-004-393B-2	US-09-004-393B-4	ID
16,	6,	6	1, 2	46,	57,	17,	45,	44,	10,	8, A	11,	15,	16,	18,	9	4, A	15,	13,	14,	12,	36,	21,	20,	19,	ρ	Sequence 4, Appli	Description

RESULT 2
US-09-004-393B-2
; Sequence 2, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
; APPLICANT: Hanson D., Andrew

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275 F-----PMECNWKVFCDNYLDSSYHVPYAH

Qy	Db Qy	Qу	Qy Db	3 tt 10	US S G G G G G G G G G G G G G G G G G		
182	131 216	71 159	11 99	Query M Best Lo Matches	US-09-004-3931 Sequence 4, Patent No. GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT FILE REFER CURRENT APPL CURRENT APPL FRIOR APPL PRIOR FILII FRIOR FILII FRIO		22666666666666666666666666666666666666
				Match Local Simi es 58;	393B- 4, A A, A INFOR NT: NT: F INV APPL COF SE CO		93 93 93 94 91 91 91 91 91 90 91 90 90 90 90 90 90 90 90 90 90 90 90 90
KVVIKAN	EVARVESE : : : PL-KVAEW	DGSIRAFLNVCRHRGK : QGELHAFHNVCTHRA-	KHLIHGDE ; ; PSTWYTEF	ilarity Conservat	i de la compania del compania del compania de la compania del compania de la compania del compania del compania del compania del compania del compania de		
KAPAE	TIAGEIY. YIEBH.	RGKTLV ::: RA-SIL	ELFQH : AFYSH	9.3%; 27.4%; ative	.on US/0), Andr. sabapath Michael Polynu- Pol		421 5588 5588 1588 1087 11087 1358 446 446 468 1693 1693 346 525 525 774
NEV	GCF	SVE : ACG	HELK - -:	# 39 # #			444422211344441244
LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213	KCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLE :	DGSTRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 	ESGLSQKHLIHGDEELFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRON : : : : : : : : : : : : : : : EDALTPPSTWYTEPAFYSHELERIFYKGWQVAGYSEQVKEKNQYFTGSLGNVEYLVSRDG	Score 224; DB 4; Le Pred. No. 6e-13; 37; Mismatches 97;	n US/09004393B , Andrew bapathi, Bala ichael Polynucleotides Encoding Choline Plants Transformed Therewith 62 UMBER: US/09/004,393B 198-01-08 BER: 60/035,147 997-01-08 er. 2.0	ALIGNMENTS	4 US-09-239-303-2 4 US-09-134-001C-4800 4 US-09-036-987A-6 4 US-09-370-700-6 2 US-08-570-311-8 2 US-08-570-311-27 1 US-07-627-539G-7 1 US-07-627-539G-7 1 US-07-627-539G-7 1 US-08-478-507-7 4 US-09-128-275A-7 4 US-09-128-275A-2 4 US-09-149-476-493 1 US-09-149-476-493 1 US-08-348-891A-2 2 US-08-905-817-2 4 US-09-276-400-7 4 US-09-276-400-7
		PFEKDLYGESLNK :: : SKATETQNLDP		446; ls 20;	Monooxygenase		Sequence 2, Sequence 6, Sequence 6, Sequence 8, Sequence 8, Sequence 27, Sequence 7, Sequence 7, Sequence 7, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 49 Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 3,
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                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MULTAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and TITLE OF INVENTION: Plants Transformed Therewith
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TYPE: PRT
                               REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Johal, Gurn APPLICANT: Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                      CITY: Charlotte
STATE: No. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 FQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SILACGSGKKSCFVCPYHGMVYGMDGSLAKASKAKP--EQNLDPXELGLVPL-KVAVWGP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVLISLDRSLEEGGDVGTEWLGTSA---EDVKAHAFDPSLQFI-HRSEFPMESNWKIFSD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSHELERIFYKGWQVAGISDQIKEPNQYFTGSLGNVEYLVSRDGEGKVHAFHNVCTHRA- 166
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                                                                                                                                                                                                                                                                                                                                 28234
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6211437
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919-881-3175
                                                                                                                                                                                                                                                                                                                                                  USA
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              919-881-3140
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Drawer 34009
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                                                         5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 223; DB 4; Pred. No. 7.3e-13;
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US-08-810-009-21

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-810-009-20
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                                                                   Matches
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                      TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SPIUILL, W. MUITTAY
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STREET: P.
                                 79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Charlotte
STATE: No. 6211437th Carolina
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                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 28234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
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                                                                   Conservative
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O. Drawer 34009
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                                                                               7.2%;
85.7%;
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                                                                                  Score 174; DB 4;
Pred. No. 7.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 185; DB 4;
Pred. No. 6.4e-11
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                   Sequence 36, Application US/09028934 Patent No. 6117670
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37,943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELERAX: 919-881-3175
TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLAN
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                       APPLICANT: APPLICANT:
                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                             CORRESPONDENCE ADDRESS: No. 6117670artis Corporation
                                                                                                           TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                            STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                    79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
   COUNTRY: UZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  1 NVCRHRGKTIVDAEAGNAKGPVCGYHGWGYGSNGK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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No. 6211437th Carolina
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                                                                                                                                                         van Pee, Karl-He
Kirner, Sabine
Young, Thomas R.
                                                                                                                                                                                                                       Ligon, James M. Hill, Dwight S. Lam, Steven T.
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                                                                                                                                                                                                         Hammer, Philip E.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168; DB 4;
Pred. No. 2.6e-09;
3; Mismatches 4
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                            US-08-810-009-12

; Sequence 12, Application US/08810009

; Patent No. 6211437
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GENERAL INFORMATION: APPLICANT: Briggs
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US-09-028-934-36
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
341
                                                                                                                                                                             260
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                                       380 DSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSN 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 IHGDEELFQ-----HELKTIFARNW-LFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/028,934 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 IRAFLNVCRHRGKTLVSVEAGNAKGFV-----CSYHGWGFGSNGELQSVPFEKDLYGES 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                              WTYAIVEKDMPEDLKRRLADSV---QRTIGPAGF----WESDDNDNMETASQNGKKYQSR 379
                                                                                                                                                                                                                     PELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEV 326
DQLIL-----KYRAFYRRWVNKVALEN
                                                                                                                                                                        -----GCIMTVSLD---GDVKYRL----LQCV------TPVDKEETVM
                                                                                                                                                                                                                                                                   PPPGQEALARDGAWFGAGIDFHVDRYFGPLGVISRTLGLSMSRMQLHFDGYPG------
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Briggs, Steven P.

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Best Local Similarity
Whiches 18; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14,
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NAME: SPIULLI, W. MUITAY
REGISTRATION UNMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
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SEQUENCE CHARACTERISTICS
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,00
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                               APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                  CURRENT APPLICATION DATA:
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STATE: No. 6211437th Carolina
                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                 ZIP: 28234
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                  CITY: Charlotte
STATE: No. 6211437th Carolina
                                                                                                                                                                                                                      STREET:
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                 APPLICATION NUMBER:
                                                                                                                                                                                                                                       ADDRESSEE:
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04-MAR-1997
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52.9%;
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                 US/08/810,009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 110; DB 4;
Pred. No. 0.00086;
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; MOLECULE TYPE: US-08-810-009-13
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US-08-810-009-13
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Query Match
Best Local Similarity
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Patent No. 6211437
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APPLICANT: Briggs,
APPLICANT: Johal,
APPLICANT: Gray,
                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 35 amino acid
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.U. STREET: P.U. CITY: Charlotte
CITY: Charlotte
NO. 6211437th Carolina
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TELEX: 575102
                                                                                                                                                                                  TELEPHONE: 919-00.
                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                          FILING DATE: 0. CLASSIFICATION:
                                                                                TOPOLOGY:
                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 4.5%;
Local Similarity 52.9%;
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version
                                                                                   linear
                                                               protein
                                                                                                                                                                                                                                                                                                                       04-MAR-1997
 4.5%;
52.9%;
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Score 108; DB 4; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109; DB 4; Pred. No. 0.0011;
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             Length 35;
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US-09-311-626B-4
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                                                                                                                              Sequence 4, Application US/09311626B Patent No. 6399347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6211437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
             APPLICANT: Andersen, Lene No. 6399347boe
APPLICANT: Schulein, Martin
APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                               APPLICANT: Jorgensen, Per Lina
APPLICANT: Schnorr, Kirk
APPLICANT: Andersen, Lene No.
APPLICANT: Schulein, Martin
APPLICANT: Outtrup, Helle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Briggs, Ste
APPLICANT: Johal, Gurn
APPLICANT: Gray, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELLEFAX: 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-00-
                                                                                                                                                                                                                                                                   79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNG 112
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 04-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/09/311,626B
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                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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US-08-810-009-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08810009 Patent No. 6211437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.5%;
Best Local Similarity 21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 61 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-05
PRIOR APPLICATION NUMBER: 060/
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bacillus licheniformis
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE: 04-MAR-19
                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 KGKVIGNANADYRNAQGRILSGPEYLTVFKG----DTGAELTTVNYEPARGNVADWGDSYG 301
                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                        STREET: P.O. Dri
CITY: Charlotte
STATE: No. 6211
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 RGKTLVSVEAG--NAKGFVCS----YHGWGFGSNGELQSVPFEK------DLYG 125
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                        6211437th Carolina
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                    04-MAR-1997
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                                                                                                                                                                                                                                                                                                           PARK & GIBSON
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TELEPHONE: 919-881-3140

REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER: ATTORNEY/AGENT INFORMATION:

Spruill, W. Murray

32,943

5718-4

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RESULT 13
US-08-810-009-18
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                                                             US-08-810-009-18
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                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18,
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    Matches
                  Best Local
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                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SPIJIL, W. MUTTBY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOTITLE OF INVENTION: CELL NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Gray, John
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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LENGTH: 35 amino acids
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                                                                                                                                                                    TELEFAX: 51.02
                                                                                                                                                                               TELEPHONE: 919 - 881-3175
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/810,009 FILING DATE: 04-MAR-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Charlotte
STATE: No. 6211437th Carolina
                                                                                         TOPOLOGY:
                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                  Similarity
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P.O. Drawer 34009
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   Conservative
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                4.3%;
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4; Mismatches
Score 104; DB 4;
Pred. No. 0.0032;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106; DB 4;
Pred. No. 0.0021;
                           DB 4; Length 35;
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   Indels
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RESULT 14
US-08-809-326A-16
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                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 224711/94
APPLICATION NUMBER: 20-SEP-1994
                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 10
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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                                         TYPE:
                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                              REGISTRATION NUMBER:
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                     TOPOLOGY:
                                                          LENGTH:
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                                                        432 amino acids
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peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                        JP 106009/95
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TITLE OF INVENTION:
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TITLE OF INVENTION:
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                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-APR-
                                                                                                                    APPLICATION NUMBER: JP 224711/94
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106006/95
                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                       CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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                       PRIOR APPLICATION DATA:
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                                                                                                     FILING DATE:
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Matsumoto, Akira
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FUSED PROTEINS CONTAINING THE POLYPEPTIDES,
THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSTIS OF CHLAMYDIA
PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNEUMONIAE GENE
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                                                           JP 106008/95
JP 106009/95
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Best Local Similarity
Watches 53; Conserva
Search completed: January 27, 2003, 09:04:58 Job time: 12.1667 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-809-326A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acid
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        119
                                                                        225 KDKTSSTT
                                                                                                           405 KSAIGETS 412
                                                                                                                                                                                  355 AGFWESDDNDNME----TASQNGKKYQSRDSD-----LLSNLGFGEDVYGDAVYPGVVG 404
                                                                                                                                                                                                                                                       300 V-----FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGP 354
                                                                                                                                                                                                                                                                                                                              247 GSGMGVLWDGYSGVHSADL------VPELMAFGGAKQERLNKEIGDVRARIYRSHLNCT 299
                                                                                                                                                                                                                                                                                                                                                                                                         195 WKAPAENFYGDAYHYGWTHASSL------RSGESIFSSLAGNAALPPEGAGLQMTSKY 246
                                                                                                                                                                                                                                                                                             67 GTDDRVTW-----VKSVDEAIAACGDVPEIMVIGGG---RVYEQFLPKAQKLYLTHIDAE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                      22 WNLPAD------LAWFKRNTLNKPVIMGRHTWESIGRPLPGR-----KNIILSSQP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Miller, Charles E. REGISTRATION NUMBER: 24,
                                                                                                                                               -----DNQKNIMSQVLTSTPQGVPQQDKLSGNETKQIQQTRQGKNTEMESDATIAGASG 224
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21.4%;
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Run on:

Title: Perfect score: Sequence: January 27, 2003, 08:54:32; Search time 25.8333 Seconds (without alignments) 3581.232 Million cell updates/sec US-09-843-250-36
2408
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
10: sp_plage:*
11: sp_rodent:
12: sp_virus:*
13: sp_virus:*
14: sp_urclas:
15: sp_virus:
16: sp_bacter:
17: sp_archea; sp_archea:*
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sp_mhc:* sp_organelle:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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277	277	277	277	277	277	277	451	447	447	447	447	447	449	449	449	Match Length		
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Q9EUC7	Q9F5S3	Q9F5S9	Q9F5S8	Q9F5T3	Q9F5S4	Q9ETK2	Q45695	Q8RTL4	P95564	Q8VUD4	052382	Q9L5D2	Q9ZI73	Q52142	Q938R9	ID		
Q9euc7 pseudomonas	Q9f5s3 pseudomonas	Q9f5s9 pseudomonas	Q9f5s8 pseudomonas	Q9f5t3 pseudomonas	Q9f5s4 pseudomonas		Q45695 burkholderi	Q8rtl4 comamonas s	P95564 pseudomonas		052382 ralstonia s	Q915d2 comamonas t	Q9zi73 pseudomonas	Q52142 pseudomonas	Q938r9 pseudomonas	Description		

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uncultured	uncultured	uncultured	ralstonia	burkholderi	napthalene	marinobacte	alcaligenes	burkholder	burkholder	pseudomona	pseudomonas	pseudomonas	pseudomonas	ralstonia	burkholderi	pseudomonas	pseudomona	pseudomona	pseudomonas									

ALIGNMENTS

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121 KDLYGESLNKKCLGLKEVARVESFHGFTYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	61 IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 	1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60 	Query Match 96.8%; Score 2332; DB 2; Length 449; Best Local Similarity 96.0%; Pred. No. 1.6e-171; Matches 431; Conservative 12; Mismatches 6; Indels 0; Gaps	SEQUENCE 449 AA; 49608 MW; 5EFEDBE0282FE812 CRC64;	057	Pfam; PF00848; Ring_hydroxyl_A; 1.	InterPro; IPR001663; Ring_hydroxyl_A.		Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AY048759: AAL07262.1:	Min KH., Ji SH.;	SEQUENCE FROM N.A.	NCBL_Tax1D=294;		Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	Pseudomonas fluorescens.	NAHAC.	(TrEMBLrel.	_	-2001 (TrEMBLrel.		O938R9 PRELIMINARY; PRT; 449 AA.	LT 1 R9

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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                       Submitted (JUN-1997) to the EMBL; AB004059; BAA20391.1; HSSP; P23094; INDO.
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Yue-Wu W., Masao F., Hohzoh K.
"The molecular malysis of NAH
Chromosomes of Pseudomonas aer
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aromatic hydrocarbon dioxygenase and polycyclic aromatic
dihydrodiol dehydrogenase in Pseudomonas putida OUS82.";
J. Bacteriol. 176:2444-2449(1994).
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Query Match
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Matches 402
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                                                                                                                                                                                                                                                                                                                          Q9ZI73;
Q9ZI73;
01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                                                                                                        "Genetic characterization and evolutionary implications of chromosomally encoded naphthalene-degradation upper pathway Pseudomonas stutzeri ANIO.";

Gene 236:149-157/1000
                                                                   Pfam; PF00355; Rieske; 1. Pfam; PF00848; Ring_hydroxyl_A; 1. PRINTS; PR000909; RNGDLOXGNASE. PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                    Gene 236:149-157(1999)
EMBL; AF039533; AAD021
HSSP; P23094; 1NDO.
                                                                                                          InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
                                                         Dioxygenase
                                                                                                                                                                                                                            STRAIN-AN10
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                            Pseudomonas
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                                              SEQUENCE
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            91.7%;
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S large subunit.
           Score
Pred.
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subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                           Query Match
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InterPro; IPR001663; Ring_hydroxyl_A.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appl. Microbiol. Biotechnol. 55:609-618(2001). EMBL; AF252550; AAF72976.1; -. HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moser R., Stahl U.;
"Insights into the genetic diversity degrading bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comamonas testosteroni (Pacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Polyaromatic hydrocarbon dioxygenase large subunit.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21306905;
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                                                                                                      MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG
                       IDEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
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                                                                         MIYEN -- LVSEAGLTQKHLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVTAKMG
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                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                    447
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                  49548 MW;
                                                                                                                                                                                                           91.1%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Pseudomonas testosteroni).
ia; beta subdivision; Comamonadaceae;
                                                                                                                                                                                27;
                                                                                                                                                                                                     Score 2193; DB 2;
Pred. No. 8.1e-161;
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  Matches
                        Query Match
                                                                                                                                                Zhou N.Y., Fuenmayor S.L., Williams P.A.;
"nag genes of ralstonia (Formerly pseudomonas)
enzymes for gentisate catabolism.";
J. Bacteriol. 183:700-708(2001).
EMBL; AF036940; AAD12610.1; -.
HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                       MEDLINE=98233751; PubMed=9573207;
Fuenmayor S.L., Wild M., Boyes A.L., Williams
"A gene cluster encoding steps in conversion
gentisate in Pseudomonas sp. strain U2.";
D. Bacteriol. 180:2522-2530(1998).
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052382;
                                                                     InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Risske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
PROSTITE; PS00570; RING_HYDROXYL_ALPHA;
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                                                  SEQUENCE
                                                              Dioxygenase; Plasmid
                                                                                                                                                                                                                          MEDLINE=20576173; PubMed=11133965;
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400; Conservative
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Score 2189; DB 2;
Pred. No. 1.6e-160;
5; Mismatches 22;
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                   Query Match
Best Local s
Matches 375
                                                            Johnson G.R., Jain R.K., Spain J.C.;

"Origins of the 2,4-dinitrotoluene pathway.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF169302; AAL50021.1; -.

R InterPro; IPR001281; Rieske.

RInterPro; IPR001663; Rieske.

R Pfam; PF00355; Rieske; 1.

R Pfam; PF00348; Ring_hydroxyl_A; 1.

R Pfam; PF00848; Ring_hydroxyl_A; 1.

R PRINTS; PR00090; RNG_HYDROXYL_ALPHA; UNKNOWN_1.

R PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.

R PROSITE; PS00570; RING_HYDROXYL_ALPHA; UNKNOWN_1.
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01-MAR-2002
01-MAR-2002
01-JUN-2002
DntAc.
                                                                                                                                                                                                                               MEDLINE-20254695; PubMed-10795678; Johnson G.R., Jain R.K., Spain J.C.; Properties of the trihydroxytoluene oxygenase from Burkholderia cepacia R34: an extradiol dioxygenase from the 2,4-dinitrotoluene pathway.";
                                                                                                                                                                                                                      Arch.
                                                                                                                                                                                                                                                                                                                                  Burkholderia cepacia (Pseudomonas cepacia). Bacteria; Proteobacteria; beta subdivision; Burkholderia.
                                                                                                                                                                                       STRAIN-R34;
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                    375; Conservative
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Last annotation
                   Score 2074; DB 2;
Pred. No. 1.2e-151;
9; Mismatches 33;
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Best Local :
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HSSP; P23094; 1NDO.
InterPro; IPRO01281; Rieske
InterPro; IPRO01663; Ring_h
Pfam; PF00355; Rieske; 1.
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P95564;
01-MAY-1997
01-MAY-1997
01-JUN-2001
ISPALPHA 2NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parales J.V., Kumar A., Parales R.E., Gibson I "Cloning and sequencing of the genes encoding dioxygenase from Pseudomonas sp. J842.";
Gene 181:57-61(1996).
                                                                                                                                                                                                                                                           Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDLOXGBASE.
PROSTTE; PS00570; RING_HYDROXYL_ALPHA; 1.
SEQUENCE 447 AA; 49485 MW; 1CB0E223E528E3BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97128768; PubMed=8973308;
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Bacteria; Proteobacteria.
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                      IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                           MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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                                                                                MSYQN--LVSEAGLTQKLLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVTAKMG 58
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Pred. No. 3e-150;
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Best Local S
Matches 369
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Lessner D.J., Johnson G.R., Parales R.E., Spain J.C., Gibson D.T.;
"Molecular Characterization and Substrate Specificity of Nitrobenzene Dioxygenase from Comamonas sp. Strain JS765.";
Appl. Environ. Microbiol. 68:634-641(2002).
EMBL, AF379638; AAL76202.1;
EMBL, AF379638; AAL76202.1;
SEQUENCE 447 AA; 49556 MW; 4CA961F99A37DF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Comamonas sp. JS765.
Bacteria; Proteobacteria;
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                                                        ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                     VDEVIVSRQNDGSVRAFLNVCRHRGKTLVHAEAGNAKGFVCGYHGWGYGSNGELQSVPFE 118
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                                            MSYQN--LVSEAGLTQKLLIHGDKELFQHELKTIFARNWLFLTHDSLIPSPGDYVKAKMG
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Pred. No. 5.1e-148;
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J. Bacteriol. 178:4926-4934(1996).
EMBL; U62430; AAB09766.1; -.
HSSP, P23094; INDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001653; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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01-NOV-1996
01-NOV-1996
01-DEC-2001
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SEQUENCE 451 AA; 49827 MW; 726796C29CEF9A10 CRC64;
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'2,4-Dinitrotoluene dioxygenase from Burkholderia
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                       FPNNCFLTGAGVFKVFNPIDENTTEAWTYAIVEKDMPEDLKRRLADAAQRSTGPAGYWES
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Query Match
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09F5T3;
01-MAR-2001
01-MAR-2001
01-DEC-2001
Naphthalene
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NON_TER
NON_TER
"Coexistence of two naphthalene dioxygenase genes "Coexistence of two naphthalene dioxygenase genes Pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ data
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Pfam; PF00848; Ring_hydroxyl_A;
PRINTS; PR00090; RNGDIOXGNASE.
                                                                     STRAIN=19IIDNH;
                                                                                     SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=139738
                                                                                                                                                       Pseudomonas sp. 19IIDNH.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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PROSITE; PS00570; RING_HYDROXYL_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2000) to the EM EMBL; AF306440; AAG25700.1; -. HSSP; P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase genes (nahAc)
Pseudomonas strains from West Mediterranean Sea.";
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01-DEC-2001
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ 115
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277
277 AA;
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(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                              PRELIMINARY;
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99.6%;
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Pred. No. 9.1e-107;
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                                                                                                                                                         subdivision; Pseudomonadaceae;
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HSSP;

AF306426; AAG25686.1; P23094; INDO.

InterPro; IPR001281; Rieske. InterPro; IPR001663; Ring_hy

Ring_hydroxyl_A.

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NON_TER
NON_TER 2
                                                                                                                                                        "Coexistence of two naphthalend dioxygenase genes (nahAc) Pseudomonas strains from West Mediterranean Sea."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF306434; AAG25694.1; -.
                                                                                                                                                                                                                                                                                                                                         Q9F5S8;
01-MAR-2001
                                                                           InterPro; IPR001281; Rieske.
InterPro; IPR001281; Rieske.
InterPro; IPR00163; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00048; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RING_HYDROXYL_ALPHA;
PROSITE; PS00570; RING_HYDROXYL_ALPHA;
                                                                                                                                                                                                                                                                                                                   01-MAR-2001
01-DEC-2001
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pfam; PF00848; Ring_hydroxyl_A; 1.
prints; PR00090; RNGDIOXGNASE.
prOSITE; PS00570; RING_HYDROXYL_ALPHA;
                                   SEQUENCE
                                                       Dioxygenase.
NON_TER
                                                                                                                                                                                                                                                                                                                                                               Q9F5S8
                                                                                                                                                                                                                STRAIN=PR3MN2;
                                                                                                                                                                                                                                                                                   Pseudomonas sp.
                                                                                                                                                                                                                                                                                                         Naphthalene
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                                                                                                                                                                                                                                                 NCBI_TaxID=139773;
                                                                                                                                                                                                                                                                      Bacteria;
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277
277 AA;
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277
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30064 MW;
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19,
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Pred. No. 1.
Score 1484; DB 2;
Pred. No. 1.8e-106;
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                 6BFF83D32F04CFC3
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SEQUENCE
                                                                                                                                                                                                                                                                                     "Ferrero M.A., Lalucat J., Bosch R.;
"Coexistence of two naphthalene dioxygenase genes (nahac)
Pseudomonas strains from West Mediterranean Sea.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF30643; AA025693.1; -.
HSSP; P23094; 1NDO.
InterPro; IPR001281; Rieske.
InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00355; Rieske; 1.
Pfam; PF00359; RNGDIOXGNASE.
PRINTS; PR00620; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9F5S9 PRELIMINARY;
O9F5S9;
01-MAR-2001 (TIEMBLrel. 16,
01-MAR-2001 (TIEMBLrel. 16,
01-DEC-2001 (TIEMBLrel. 19,
                                                                                                                                                                                                                                                    Dioxygenase.
                                                                                                                                                                                                                                                                             PROSITE; PS00570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=139736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas sp.
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                                                                                                                                    TAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQ 115
                                                                       SVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFK 175
EGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSH
                                      HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
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                         HSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPP
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nilarity 99.6%;
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les 1;
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Search completed: January 27, Job time: 27.8333 secs
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Q9F5S3;
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01-MAR-2001
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NON_TER
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SEQUENCE 27
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**Coexistence of two naphthalene dioxygenase genes (nahac)
**Pseudomonas strains from West Mediterranean Sea.";
**Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
**EMBL; AF306441; AAG25701.1; -.
**HSSP; P23094; 1NDO.
**InterPro; IPR001281; Rieske.
**InterPro; IPR001663; Rieske.**
**InterPro; IPR01663; Rieske.**
**InterPro; IPR01664; Rieske.**
**InterPro; IPR01664; Rieske.**
**InterPro; IPR01664; Rieske.**
**InterPro; IPR01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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STRAIN-SIIANH;
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277 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
dioxygenase iron sulfur protein 1 (Fragment).
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277
30062 MW; 82C78D865A92D0AB CRC64;
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GenCore version 5.1.3 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 08:47:32; Search time 7.16667 Seconds (without alignments) 2598.540 Million cell updates/sec

Title: Perfect score: Sequence: US-09-843-250-36
2408
1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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405	849	849	428	985	1693	420	847	518	452	350	331
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P51851 pisum sativ	Q62936 rattus norv	P70175 mus musculu	P28868 candida alb	Q12558 aspergillus	Q04610 hepatitis e	O59650 pyrococcus	Q9bzfl homo sapien			Q9y3f4 homo sapien	

ALIGNMENTS

~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	RESULTATION OF THE STATE OF THE
SPECIES-P. putida; STRAIN=NCIB 9816; Parales J.V., Parales R.E., Kumar A., Gibson D.T.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. STRAIN-C18; MEDLINE-94042852; PubMed-8226631; Denome S.A., Stanley D.C., Olson E.S., Young K.D.; Metabolism of dibenzothicphene and naphthalene in Pseudomonas strains: complete DNA sequence of an upper naphthalene catabolic pathway."; J. Bacteriol. 175:6890-6901(1993). [4] SEQUENCE FROM N.A. SPECIES-P. putida; STRAIN-G7 / ATCC 17485; PLASMID=NAH7; SEQUENCE FROM N.A., Osslund T.D., Saunders R., Ensley B.D., Suggs S., Harcourt A.A., Suen WC., Cruden D.L., Gibson D.T., Zylstra G.J.; "Sequences of genes encoding naphthalene dioxygenase in Pseudomonas putida strains G7 and NCIB 9816-4."; Gene 127:31-37(1993). [5] SEQUENCE FROM N.A. SPECIES-P. putida; STRAIN-BS202; PLASMID=NPL1; Bezborodnikov S.G., Boronin A.M., Tiedje J.M.; "Nucleotide sequences of genes encoding an upper pathway of naphthalene metabolism of NPL1 plasmid from Pseudomonas putida strain BS202."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. [6]	SEPU DOB_PSEPU DOB_PSEPU 23094; Q5212. 1-NOV-1991 (! 1-NOV-1991 (! 5-JUN-2002 (!) aphthalene 1. 2-dioxygenas DOB NAHAC Seudomonas SI Seudomonas SI 1-Seudomonas SI Seudomonas SI 1-Seudomonas SI CBI_TaxID=30: CBI_TaxID=30: CBI_TaxID=30: CBI_TaxID=30: CGI_TaxID=30: CGI_T

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METAL
VARIANT
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InterPro; IPRO01281; Rieske.
InterPro; IPRO01663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: Naphthalene + NADH + O(2) = (1R,2S)-1,2-dibytronaphthalene-1,2-diol + NAD(+),
-!- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-!- PATHWAY: UPPER NAPHHALENE CATABOLIC PATHWAY WHICH INVOLVES
CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF
DIBENZOTHIOPHENE (DBT) AND PHEMANTHRENE. CONVERTS PHENANTHRENE TO
1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DBT IS LIMITED TO
OXIDATION OF THE AROMATIC RING.
-!- SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME
SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT IS COMPOSED
OF FERREDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS
COMPOSED OF AN HEXAMER OF THREE LARGE ALPHA SUBUNITS (NDOB) AND
THREE SMALL BETA SUBUNITS (NDC).
-!- SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                      METAL
                                                                                                                                                               METAL
                                                                                                                                                                             METAL
                                                                                                                                                                                                   PRINTS; PR00090; RNGDIOXGNASE.
PROSITE; PS00570; RING_HYDROXYI_ALPHA; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
SPECIES=P.putida; STRAIN=NCIB 9816;
MEDLINE=98298434; PubMed=9634695;
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Structure 6:571-586(1998)
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SPECIES=P.putida; STRAIN-ATCC
                                                                                                                                                                                        Dioxygenase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kauppi B., I
Ramaswamy S.
                                                                                                                                                                                                                                                                                                           BL; M23914; AAB47591.1; -.
BL; M60405; AAA16125.1; -.
BL; M83949; AAA25902.1; -.
BL; M83949; AAA25902.1; -.
BL; AF010471; AAB62707.1; -.
BL; AF004284; AAB61373.1; -.
BL; JS0071; JS0071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encuropean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CISNAPHTHALENE DIHYDRODIOL.
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007824;
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15-DEC-1998
15-JUN-2002
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                                  Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)

-MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION
BOTH ATOMS OF MOLECULAR OXYGEN INTO NAPHTHALENE TO FORM CIS-
                                                                                                              Hamann C
                                                                                                                             STRAIN-ATCC
                                                                                                                                                                                   NCBI_TaxID=294;
                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                          Plasmid
                                                                                                                                                                                                                                                           Pseudomonas
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5-JUN-2002 (Rel. 41, Last sequence update)
aphthalene 1,2-dioxygenase alpha subunit (EC
.2-dioxygenase ISP alpha).
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   NAPHTHALENE DIHYDRO CATALYTIC ACTIVITY:
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-:- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.

-:- PATHWAY: UPPER NAPTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPTHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHIOPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO 1-HYDROXY-2-NAPTHOIC ACID AND THE METABOLISM OF DBT IS LIMITED TO OXIDATION OF THE AROMATIC RING.

-:- SUBUNIT: NAPHTHALENE DIOXYGENASE (NDO) MULTICOMPONENT ENZYME SYSTEM IS COMPOSED OF AN ELECTRON TRANSFER COMPONENT AND AN IRON SULFUR PROTEIN (ISP). THE ELECTRON TRANSFER COMPONENT IS COMPOSED OF FERREDOXIN REDUCTASE (NDOR) AND FERREDOXIN (NDOA), AND ISP IS OTOMPOSED OF A LARGE ALPHA SUBUNIT (NDOB) AND A SMALL BETA SUBUNIT
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF004283; AAB61370.1; HSSP; P23094; 1NDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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                      361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
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                    DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                  FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWES
                                                                                                                                                                    QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                      ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSIRSGESIFSSLAGNAALPPEGAGL 240
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                                                                                                                                                                                                                                  ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRTGESIFSSLAGNAVLPPEGAGL
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FPNNSVLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADAVQRTFGPAGFWES
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nilarity 95.5%;
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IRON (BY SIMILARITY).

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IRON (BY SIMILARITY).
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Pred. No. 1.3e
2; Mismatches
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Pfam; PF0084B; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                EMBL; D84146; BAA12240.1; -. HSSP; P23094; INDO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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Kiyohara H.;
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15-JUN-2002 (Rel. 41, Last annotat
Naphthalene 1,7-dioxygenase alpha
1,2-dioxygenase ISP alpha).
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FUNCTION: COMPONENT OF NAPHTHALENE DIOXYGENASE (NDO)
MULTICOMPONENT ENZYME SYSTEM WHICH CATALYZES THE INCORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
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HCAE OR PHOC1 OR HCAA OR HCAA1 OR DIGA OR B25:
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Turlin E.,
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                                                                                                                          Blattner F.R., Plunkett G. III, Blookiley M., Collado-Vides J., Glasner
                                                                                                                                                                        STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                         complete genome sequence of nce 277:1453-1474(1997).
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AX Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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pfam; pF00848; Ring_hydroxyl_A; 1.

pRINTS; pR00909; RNGDIOXGNASE.

pROSITE; pS00570; RING_HYDROXYL_ALPHA; 1.

Aromatic hydrocarbons catabolism; Oxidoreductase;
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InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
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DNA Res. 4:91-113(1997).
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MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                          AE005484; AAG57651.1; -. AP002562; BAB36827.1; -. P23094; INDO.
                                                                                                                                                                                                                                                                                                                                                                                         D90883; BAA16433.1; -. D90884; BAA16441.1; -.
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01-NOV-1995 (Rel. 32, La
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Benzene 1,2-dioxygenase
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                                                        Tan H.-M., Tang H.-Y., Joannou C., Abdel-Wahab N.H., Mason J.R.; "The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenase are unusual in codon usage and low in G+C content."; Gene 130:33-39(1993).
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CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-dihydrobenzene-1,2-dio1 + NADH + O(2) = cis-1,2-COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. PATHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.
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                                                                                                            PubMed=8344526;
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V-> A (IN RDE: 1).
V-> A (IN RDE: 1).
GHRARNSKICLEMGIGOEKRRDDGIPGITNYIPSETAARGM YORWADLLSSESWOEVLDKTAAYQOEVMK -> ATAPATAN CVWKWGLVRKSAATTAFLALLTISFQKLPLVECTNAGPIF (IN REF: 1).
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                                                                                                                                                                                              subdivision; Pseudomonadaceae;
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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InterPro; IPR001663; Ring_hydroxyl_A.
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SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no reserve by non-profit institutions as long as its content
                                                                                                                            PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWESD
                                                                                                                                                                                                                                                WKAPAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVL
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                           AHVSSSNW
                                                      DGENWVEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
                                                                                 DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ
                                                                                                                                                                   {\tt WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF}
                                                                                                                                                                                                WDGY-SGVHSAD------LVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVF
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                                                                                                             PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
                                                                                                                                                                                                                              WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP-----KFGKQYRAS
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IRON-SULFUR (2FE-2S) (BY S)
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Pred. No. 8.3e-44;
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RESULT 6
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15-JUN-2002
Toluene 2,3-
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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Bacteria; Proteobacteria;
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InterPro; IPR001663; Ring_hydroxyl_A.
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HSSP; P23094; 1NDO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               todC1C2BADE genes and their expression Biol. Chem. 264:14940-14946(1989).
VLWDGYSGVHSADLVPELMAF - - GGAKQERLNKEIGDVR - - ARIYRSHLNCTVFPNNSML
                           WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                             WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                               PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                                 --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN
                                                                                                                                     QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----CLNKKEWS
                                                                                                                                                    VCRHRGKTLYSYEAGNAKGFYCSYHGWGFGSNGELQSYPFEKDLYGESLNKKCLGLKE---
                                                                                                                                                                                        IYTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVVRQKDASIAVFLN
                                                                                                                                                                                                               IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
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145; Conserv
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90 (Rel. 13, Last sequence update)
92 (Rel. 41, Last annotation update)
,3-dioxygenase alpha subunit (EC 1.1
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IRON (BY SIMILARITY).
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                                                                                                                                                                                                                                         Score 650.5; DB 1
Pred. No. 1.2e-43;
1; Mismatches 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BPHA_BURCE
P37333;
01-OCT-1994
                                                                                                                                                                                                                                    Haddock J.D., Gibson D.T.;

J. Bacteriol. 178:2158-2158(1996).

-:- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-
phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).

-:- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per subunit.

-:- PATHWAY: Biphenyl-polychlorinated biphenyl degradation pathwa
                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequencing and transcriptional mapping of the encoding biphenyl dioxygenase, a multicomponent polychlorinated-biphenyl-degrading enzyme in Pseudomonas s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia cepacıa (rəco
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURCE
              EMBL; M86348;
                                                                                                                                                                                                                                                                                                                                               "Purification and characterization of the oxygenase component of biphenyl 2,3-dioxygenase from Pseudomonas sp. strain LB400."; J. Bacteriol. 177:5834-5839(1995).
                                                                                                                                                                                                                                                                                                                                                                                           Haddock J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-LB400;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92234948; PubMed=1569021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burkholderia
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                                                     entities
                                                                                                                                                                                                                                                                                                                          ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96011369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erickson B.D., Mondello F
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                                     send
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 174:2903-2912(1992).
                                                                                                                                                   SUBUNIT: Heterohexamer consisting of three BphA subunit: BphE subunits. A ferredoxin (BphF) and a ferredoxin red (BphG) must be present to obtain activity. SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                          first step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DΨ
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                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429
                                                                     and this statement is not removed.
                                                     requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
              AAB63425.1;
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eria; beta subdivision;
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MEDLINE=97045812;
Sylvestre M., Siro
                         STRAIN-B-356;
                                                                      Comamonas testosteroni (F
Bacteria; Proteobacteria;
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INIT_MET
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PROSITE; PS00570; RING_HYDROXYL_ALPHA;
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InterPro; IPR001281; Rieske.
InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
Pfam; PF00848; Ring_hydroxyl_A; 1.
                                   SEQUENCE FROM
                                                           NCBI_TaxID=285;
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| ||: ||| |||| : :||||| | |||||| : :
| DKSIKVFLNQCRHRGWRICRSDAGNAKAFTCSYHGWAYDIAGKLVNVPFEKEAFCDKKEG 148
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alpha subunit (EC 1.14.12)
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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IRON (BY SIMILARITY).
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in entities requires a license agreeman.

Usage horizontal institution as long as its content is in entities requires a license agreeman.
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001663; Ring_hydroxyl_A.
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-i- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-
phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-i- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron atom per su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BphE subunits. A ferredoxin (BphF) and a ferredoxin reduct (BphG) must be present to obtain activity (By similarity). SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
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FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGETSYR
                                                   --TVFPTCSFLPGINTIRTWHPRGPNEVEVWAFVLVDADAPEDIKEEFRLQNIRTFNAGG
                                                                                                                                                                                                                                                  CNWKFAAEQFCSDMYHAGTMSHLSGVLAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEV-
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                                                                                                 NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAG
                                                                                                                                                                                                  SGMGVLWDGY----
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                                                                                                                                                                                                                                                                                                                                                                                            ----ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIK 192
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                                                                                                                                              NQFRSAWGGHGAGWFINDSSILLSVVGPKITQYWTQGPAAEKAARRVPQLPILDMFGQHM
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IIT: Heterohexamer consisting of three subunits. A ferredoxin (BphF) and                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
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                                                                 Query Match
Best Local S
Matches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92165849; PubMed-1537863;
Taira K., Hirose J., Hayashida S., Furukawa K.;
Taira K. of bph operon from the polychlorinated biphenyl-degrading strain of Pseudomonas pseudoalcaligenes KF707.";
J. Biol. Chem. 267:4844-4853(1992).
-!- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = (2R,3S)-3-phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-!- CERCTOR: Binds 1 ZFe-2S cluster and 1 iron atom per subunit (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence
15-JUN-2092 (Rel. 41, Last annotati
Biphenyl dioxygenase alpha subunit
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Q52028;
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                                                                                                                                                       SEQUENCE
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Bacteria; Proteobacteria; gamr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Heterohexamer consisting of three BphA subunits and temper subunits. A ferredoxin (BphF) and a ferredoxin reductase (BphG) must be present to obtain activity (By similarity).

SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           first step.
SUBUNIT: Heterohexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Biphenyl-polychlorinated biphenyl degradation
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                                                                                                                                                                                                                                                                                                                                                                PF00848; Ring_hydroxyl_A; 1.
s; PR00090; RNGDIOXGNASE.
                                                                 al Similarity
147; Conser
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                                                                                                                                                                                                                                                                                                                                            PS00570; RING_HYDROXYL_ALPHA; 1.
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IPR001663; Ring_hydroxyl_A.
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annotation updat
subunit (EC 1.14
                                                                                     Score 617; 1
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); Mismatches
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C 1.14.12.18)
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RESULT 10

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01-NOV-1988
15-JUL-1999
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modified
                                                                                                                                                                                          This SWI
                                                                                                                                                                                                                                                                                                                                   MEDLINE=88032840; PubMed=3667527;
Irie S., Doi S., Yorifuji T., Takagi M., Yano K.;
"Nucleotide sequencing and characterization of the genes encoding benzene oxidation enzymes of Pseudomonas putida.";

J. Bacteriol. 169:5174-5179(1987).

-i- CATALYTIC ACTIVITY: Benzene + NADH + O(2) = cis-1,2-
-i- CATALYTIC ACTIVITY: Benzene + NAD(+).

-i- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-i- COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM.
-i- PATHWAY: FIRST STEP OF DEGRADATION OF BENZENE TO CATECHOL.
-i- SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF FOUR PROTEINS:
                        EMBL; M17904; AAA25735
PIR; A29830; A29830.
                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida.
Bacteria; Proteobacteria;
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                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                       DIOXYGENASE ALPHA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                               SIMILARITY:
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                                                                                                                                                                                                                                                                                                                    TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (BNZA AND BNZB),
                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYAEEAARGMYHHWMRMMSEPSWA
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15-JUL-1998 (Rel. 36, I
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Fukuda M., Yas
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MEDLINE=94324977; PubMed=8048958;
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PROSITE; PS00570; RING_HYDROXYL_ALPHA;
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PF00848; Ring_hydroxyl_A; 1.
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IPR001663; Ring_hydroxyl_A.
        Yasukouchi Y., Kikuchi Y., Nagat
., Takagi M., Yano K.;
ation of the bphA and bphB genes
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degradation of biphenyl and
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-!- CATALYTIC ACTIVITY: Biphenyl + NADH + O(2) = phenylcyclohexa-3,5-diene-1,2-diol + NAD(+).
-!- COFACTOR: Binds 1 2Fe-2S cluster and 1 iron a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Aromatic hydrocarbons catabolism; Oxide
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InterPro; IPR001663; Ring_hydroxyl_A.
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  SYRGFYRAYQAHVSSSNW
                                                                                                  PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSA--IGET
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                                               AGGTFEQDDGENWVEIQRGLRGHKAKSAPLCAQMGLNVPNKSNPDFP---GKTAYVYAEE
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Pred. No. 1.2e-38;
5; Mismatches 174; Indels
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Matches 105
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Pfam; PF00848; Ring_hydroxyl_A; 1.
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InterPro; IPR001663; Ring_hydroxyl_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=92155191; PubMed=1740120;
                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                              Dioxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00570; RING_HYDROXYL_ALPHA; Aromatic hydrocarbons catabolism; Oxido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00090; RNGDIOXGNASE
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r. J. Biochem. 204:113-120(1992).
- COPACTOR: PROBABLY BIND?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATOM. PATHWAY: DEGRADATION OF BENZOATE AND TOLUATE TO CAFECHOL. SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF THREE PROTEIT TWO SUBUNITS OF THE HYDROXYLASE COMPONENT (XYLX AND XYLY) ELECTRON TRANSFER COMPONENT (XYLZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING DIOXYGENASE ALPHA SUBUNIT FAMILY.
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HRGATLCRFRSGNKATHTCSFHGWTFSNSGKLLKVKDPKGAGYPDSFD--CDGSHDLKKV
                                     HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKKCLG---LKEV 138
                                                                                DPRLFDLEMKHIFEGNWIYLAHESQIPEKNDYYTTQMGRQPIFITRNKDGELNAFVNACS
                                                                                                                          DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR 82
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Pred. No. 8.5e-2
54; Mismatches 1
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Pfam; PF00848; Ring_hydroxyl_A; 1.
PRINTS; PR00090; RNGDIOXONASE.
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Submitted (DEC-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequences of the Acinetobacter calcoaceticus benABC for benzoate 1,2-dioxygenase reveal evolutionary relationships multicomponent oxygenases.";
J. Bacteriol. 173:5385-5395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neidle E.L., Hartnett
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MEDLINE=91358314; PubMed=1885518;
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Benzoate 1,2-dioxygenase alpha subunit (EC 1.
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Aromatic hydrocarbons
                                                                                            PIR; S23477;
                                                                                                         EMBL; AF009224; AAC46436.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.
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SUBUNIT:
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EMBL; AP002558; BAB35934.1; --
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METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C. G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe IIda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaz Kuhara S., Shiba T., Hattori M., Shinagawa H.; Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.", DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C Yamamoto Y., Horiuchi T.; ** A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage materials and the sequence of the secherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage materials and the sequence of the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isonc Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T. Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene; EG13509; yeaW.
InterPro; IPR001281; Rieske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=0157:H7 / E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the 40.1 DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
NAD; Complet
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00570; RING_HYDROXYL_ALPHA;
Hypothetical protein; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21156231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97251358;
                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: PROBABLY BINDS A 2FE-2S GROUP AND AN IRON ATO SUBUNIT: PROBABLE HETERODIMER OF YEAW AND YEAX.
SIMILARITY: BELONGS TO THE BACTERIAL RING-HYDROXYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIOXYGENASE ALPHA SUBUNIT FAMILY.
DQNAFEHEKENVFAKSWICVAHSSELANANDYVTREIIGESIVLVRGRDKVLRAFYNVCP 90
                                               DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
                                                                                                                                                                                                                                                                                                                                                                                    Complete
                                                                                                                         Similarity
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374 AA; 42:
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                                                                                                                                                                                                      42561 MW;
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IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                                               Score 249; DB Pred. No. 3.2e
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No. 3.
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.2e-12;
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Wada C.,
                                                                                                                                                                                                                                                                          Y SIMILARITY).
Y SIMILARITY).
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Tobe T.,
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                                                                                               Gaps
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RESULT 15
CHMO_AMATR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q93XE1;
15-JUN-2002 |
15-JUN-2002 |
15-JUN-2002 |
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: Choline + 2 reduced ferredoxin + O(2)
betaine aldehyde + 2 oxidized ferredoxin + H(2)O.
-!- COFACTOR: Magnesium. Probably binds a 2Fe-2S group and an
atom (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast strong (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast strong (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Meng Y.L., Wang Y.M., Zhang B., Nii N.;
"Isolation of a choline monooxygenase cDNA clone from Amaranthus tricolor and its expressions under stress conditions.";
Cell Res. 11:187-193(2001).
-i- FUNCTION: Catalyzes the first step of the osmoprotectant glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eucaryophyllidae; Caryophyllides; Amaranthaceae; Amaran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Choline monooxygenase, Chloroplast precursor (EC 1.14.15.
                                 Pfam; PF00355; Rieske; 1.
Monooxygenase; Oxidoreductase; Chloroplast; Iron-sulfur; Iron;
                                                                                             EMBL; AF290974; AAK82768.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21520075; PubMed=11642403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amaranthus tricolor (Tampala)
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                                                                            nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                 betaine synthesis.
CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                                                    INDUCTION: By salt, drought and heat stress.
SIMILARITY: BELONGS TO THE CHOLINE MONOOXYGENASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRGHQLLSGE-GKAKNVITCPYHAWAFKLDGNLAHARNCENVANFDSDKAQL---VPVRL
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                                                                          IPR001281; Rieske.
   Transit peptide.
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CHLOROPLAST (BY SIMILARITY).
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                                                                                                             KKCLGLKEVARVESFHGFIYGCFDQEAPP-----LMDYLGDAAWYLEPMFKHS--GGLEL
                                                                                                                                     GQGKVHAFHNVCTHRA-SILACGTGKKSCFVCPYHGWVFGLDGSLMKATKTEN---QVFD
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                                                                                                                                                                                                      SESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQ 69
                                             IN-RSEFPMESNWKVFCDNYLDSAYHVPYAH 295
                                                                                         PKELGLVTL-KVAIWGPFVLISLDRSGSEGTEDVGKEWIGSCA---EEVKKHAFDPSLQF
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                                                                                                                                                                                                                                       9.9%; Score 239.5; DB 1 28.4%; Pred. No. 2.2e-11;
          2003,
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IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON-SULFUR (2FE-2S) (BY SI
IRON (POTENTIAL).
IRON (POTENTIAL).
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           08:59:43
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Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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OM protein - protein search, using sw model

Run on: January 27, 2003, 08:55:37; Search time 13.1667 Seconds (without alignments) 3278.305 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-843-250-36 2408

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

283224 segs, 96134422 residues

Searched:

283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	O	5	4	ω	2	1		Result
315.5	333	341.5	391	394	409.5	410.5	416	452	587	588.5	605	617	617	617.5	639	650.5	652.5	725.5	737	737	737	774	957	2056	2292	2346	2404	2404		
13.1	13.8		16.2			17.0		18.8	24.4	24.4	25.1	25.6	•	25.6	•	27.0	27.1	30.1	30.6	30.6	30.6	32.1	39.7	•	95.2	97.4	99.8	99.8		Query
391	426	424	464	461	455	454	471	469	458	448	431	458	457	459	461	450	450	455	453	453	453	450	459	447	449	449	462	449	Ferra Cri	
2	N	Ν					N	N	Ν	<u>, </u>	N	_	Н	-				N			Ν			N	N	N	2	2		ğ
T31251	T31278	E83384	G83331	S23477	E83332	A41659	T31281	T50934	JC2467	A29830	JW0098	A42409	JC4993	B41858	S51757	A36516	JN0812	T31258	G85898	D91054	A65031	T31256	T31134	JC5352	C55217	JN0644	S27632	JS0071		,
aromatic oxygenase		probable ring-hydr	\vdash	probable benzoate	toluate 1,2-dioxyg		benzoate 1,2-dioxy	dioxygenase DitA1,	_	benzene 1,2-dioxyg	Œ				\mathbf{L}	toluene dioxygenas	\vdash	O	щ			terminal oxygenase	naphthalene dioxyg	_	Ð	naphthalene 1,2-di		naphthalene dioxyg	TOTAL	

45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30
186	214.5	223	224	233.5	249	249	249	252.5	268	270.5	283	287	296	311.5	311.5
7.7	8.9	9.3	9.3	9.7	10.3	10.3	10.3	10.5	11.1	11.2	11.8	11.9	12.3	12.9	12.9
426	186	439	446	382	374	374	374	374	420	404	415	412	429	468	468
2	Ν	N	2	N	2	N	Ν	2	N	2	2	N	N	N	2
T08550	JC5354	T09214	T14542	G70946	B64941	G90942	C85791	AF0304	T31285	н87635	AG3320	H95311	F82970	AH2665	G97447
choline monooxygen	2-nitrotoluene dio	choline monooxygen	choline monooxygen	probable dioxygena	probable choline m	probable choline m	probable choline m	probable dioxygena	biphenyl dioxygena	Rieske 2Fe-2S fami	benzoate 1,2-dioxy	probable aromatic-	probable ring hydr	ring hydroxylating	hypothetical prote

ALIGNMENTS

aphthalene dioxygenase (EC 1.14.12) ndoB protein - Pseudomonas putida C; Species: Pseudomonas putida C; Species: Pseudomonas putida C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999 C; Accession: 350071 R. Kurkela, S.; Lehyaeslaiho, H.; Palva, E.T.; Teeri, T.H. Gene 73, 355-362, 1998 A. Facierone, number: JS0070; MUID:89211973; PMID:3243438 A. Residues: 1-449 - KURP A. Accession: JS0071 A. Rocicule type: DNA A. Cross-references: GB Mx2914; NID:8151392; PIDN:AAB47591.1; PID:9151394 A. Cross-references: GB Mx2914; NID:8151392; PIDN:AAB47591.1; PID:9151394 A. Cross-references: GB Mx2914; NID:8151392; PIDN:AAB47591.1; PID:9151394 A. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B A. Gene: 100B A. Gene: 100B A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:3243438 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:32434348 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:33444 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:33444 A. Gene: 100B B. Cross-references: GB Mx2914; NID:89211973; PMID:34449; BB Mx2914; NID:89211973; PMID:34449; BB Mx2914; NID:89211973; PMID:34449; BB Mx2914; NID:89211973; PMID:3444, NID:89211973; PMID:34449; B
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A; Molecule type: DNA
A; Residues: 1-462 <DENS
A; Cross-references: EMBL:M60405
A; Cross-references: EMBL:M60405
A; Cross-references: EMBL:M60405
A; Cross-references: EMBL:M60405
A; Stanley, D.C.; Olson, E.S.; Young, K.D.
J. Bacteriol. 175, 6890-6901, 1993
A; Title: Metabolism of dibenzothiophene and naphthalene in Pseudomonas
A; Title: Metabolism of dibenzothiophene and naphthalene in Pseudomonas
A; Title: Metabolism of dibenzothiophene and naphthalene in Pseudomonas
A; Title: Metabolism of dibenzothiophene and naphthalene in Pseudomonas
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A; Title: Metabolism of dibenzothiophene and naphthalene in Pseudomonas
A; Title: Metabolism of dibenzothiophene
A; Title: Metabolism of dibenzo
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C;Species: Pseudomonas sp.
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text.
C;Accession: S27632; B49343
R;Denome, S.A.; Young, K.D.
submitted to the EMBL Data Library, February 1992
A;Description: Cloning and molecular characterization of A;Reference number: S27631
A;Accession: S27631
A;Accession: S27631
A;Status: preliminary
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Best Local :
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les 448; Conserv
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         QAHVSSSNWAEFEHASSTWHTELTKTTDR
                                                   QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                            DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                           DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                     FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWES
                                                                                                                                                                                                              FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWES
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                                                                                                                                                                                                                                                                                                  QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
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Pred. No. 4.2e-184;
0; Mismatches 1;
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R;Simon, M.J.; Osslund, T.D.; Ss
Gene 127, 31-37, 1993
A;Title: Sequences of genes ence
A;Reference number: JN0640; MUII
A;Accession: JN0644
R:Takizawa, N.; Kaida, N.; Torigoe, J. Bacteriol. 176, 2444-2449, 1994 A;Title: Identification and characte A;Reference number: A55217; MUID:94A;A;Accession: C55217
                                                                                                                                                                                                         RESULT
C55217
                                                                                                               polycyclic aromatic hydrocarbon dioxyge
c;Species: Pseudomonas putida
C;Date: 05-May-1995 #sequence_revision
C;Accession: C55217
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A; Residues: 1-449 <SIM>
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96.7%;
                           characterization of genes encoding MUID:94209249; PMID:8157615
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Pred. No. 1
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                                                                                          Moritani,
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nes 5;
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A;Gene: nahAc C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; C;Keywords: 2Fe-2S; heterotetramer; metalloprotein; oxidoreductase; Rieske in F;71-119/Domain: Rieske [2Fe-2S] homology <RSK> F;81-119/Domain: Rieske [2Fe-2S] homology <RSK His, Cys, His, Cys, His) (covalent)
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naphthalene 1,2-dioxygenase (EC 1.14.12.12) iron-sulfur oxygenase component large N;Alternate names: nahAc protein C;Species: Pseudomonas putida C;Date: 31-Dec-1993 **sequence_revision 31-Dec-1993 **text_change 20-Aug-1999 C;Date: 31-Dec-1993 **sequence_revision 31-Dec-199
                                                                                                                                                                                                                                                                                          FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWES
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DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                          DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                               FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGSKQERLNKEIGDVRARIYRSHLNCTV
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R.Parales, J.V.; Kumar, A.; Parales, R.E.; Gibson, D.T. Gene 181, 57-61, 1996
A.Title: Cloning and sequencing of the genes encoding 2-nitrotoluene A.Reference number: JC5350; MUID:97128768; PMID:8973308
A.A.C. JC5352
                                                                                                                                                                  A;Cross-references: GB:U49504; NID:g1773273; A;Experimental source: strain JS42 C:Comment: This enzyme catalyzes the addition C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                         C:Species: Pseudomonas sp.
C:Date: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Aug-1999
C:Accession: JC5352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A,Residues: 1-449 <TAK>
A;Cross-references: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
A;Cross-references: GB:AB004059; GB:D16629; NID:g2189972; PIDN:BAA20391.1; PID:g391844
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [2FG
C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;71-119/Domain: Rieske [2Fe-2S] homology <RSK>
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status pre
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JC5352
                                                                                                                                                    A; Gene:
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-447 <PAR>
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Pred. No. 3.5e-175;
13; Mismatches 12;
Pred. No. 2.56
4; Mismatches
                     Score 2056;
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R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thus submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb cat.
A;Reference number: Z20992
A;Roference number: Z20992
A;Roference number: Z20992
A;Roference: Preliminary; translated from GB/EMBL/DIA;Status: preliminary; translated from GB/EMBL/DIA;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-459 <ROM>
A;Residues: 1-459 <ROM>
A;Gross-references: EMBL:AF079317; NID:93378261;
C;Genetics:
A;Gene: bphAlf
A;Genome: plasmid pNL1
C;Superfamily: toluene dioxygenase terminal oxyge
C;Keywords: 2Fe-25; metalloprotein; oxidoreductas
F;80,82,100,103/Binding site: 2Fe-25 cluster (Cy
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C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Keywords: 2re-2S; metalloprotein; Rieske iron-sulfur protein
F;81,83,101,104/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
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A; Residues: 1-450 < ROM>
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A;Description: Complete sequence of a 184 kb catabolic
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                                                                                                                                                        -GLSVAGMNGHMVLSALDGVSGYAFYPDPKPILEYLEANRQTVIDRLGEVRGRQVWGAQV
                                                                                                                                                                                       AGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR-IYRSHL
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Pred. No. 6.6e-54;
8; Mismatches 184
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A;Molecule type: DNA
A;Rosidues: 1-19; A', 21-383, 'ATAPATANCYWKW', 397-398,451,'R',453, 'SAATTAFLALLTISFQKLPL
A;Cross-references: EMBL:237966; NID:g550595; PIDN:CAA86018.1; PID:g550596
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
F;75-123/Domain: Rieske [2Fe-2S] homology <RSK>
F;85,87,105,108/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_c C;Accession: A65031; S49592 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: A65031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, September 1994
A;Description: Cloning and sequencing of an E. coli gene homologous
A;Reference number: S49292
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A65031
biphenyl dioxygenase (EC 1.14.-.-) terminal oxygenase component large chain C:Species: Escherichia coli
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A; Residues: 1-453 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCRHRAMRVSYADCGNTRAFTCPYHGWSYGINGELIDVPLEPRAYPQGLCKSHWGLNEVP 143
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ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
                                               YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK
                                                                                                                                               GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS 412
                                                                                                                                                                                                    AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
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12, substrain MG1655
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D91054
biphenyl dioxygenase (EC 1.14.-.-) termin C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 1f C;Accession: D91054
R;Hayashi, T.; Makino, K.; Ohnishi, M.;
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DNA Res. 8
                                                                                                                                biphenyl dioxygenase (EC 1.14...) terminal oxygenase component C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: G85998
R;Perna, N.T.; plunkett III, G.; Burland, V.; Mau, B.; Glasner,
                                                                                       iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; D. Nature 409, 529-533, 2001
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A;Gene: ECs3404
C;Superfamily: toluene dio:
C;Keywords: oxidoreductase
A; Molecule t
A; Residues:
                                A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: G85898 A;Status: preliminary
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A;Residues: 1-453 <HAY>
A;Residues: 1-453 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36827.1; PID:g13362875;
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                           YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVESYKGLIFGNWDTSAPGLRDYLGDIAWYLDGMLDRREGGTEIVGGVQKWVINCNWKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                               GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA
                                                                                                                                                                                                                                                                                                                                                                                              GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS
                                                                                                                                                                                                                                                                                                                                                                                                                               AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE-----AEQRLGEVRALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKAP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCRHRAMRVSYADCGNTRAFTCPYHGWSYGINGELIDVPLEPRAYPQGLCKSHWGLNEVP
                                                                                                                                                                                                                                                                                           ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AENFVGDAYHVGWTHASSL-------RSGESIFSSLAGNAALP------
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 type: I
: 1-453
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Pred. No. 6e-51;
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                                                                                                                    Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kurokawa, K.;
Shiba, T.; Hai
                                                                                                                                                                                                                                                                                           453
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                                                                                                                  Glasner,
anta, E.;
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                                                                                                                                  J.D.; Rose,
                                                                                                                                                                      31-Dec-200
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                                                                                                                    Potamousis,
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A;Cross-references: GB:AE005174; NID:g12516944; PIDN:AAG57651.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Genetics: A;Genetics: C;Superfamily: toluene dioxygenase terminal oxygenase component C;Keywords: oxidoreductase
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                                                                                                                                           GPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETS 412
                                                                                                                                                                           AGHNN--IFPTLSWLNGTATLRVWHPRGPDQVEVWAFCITDKAASDEVKAAFENSATRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                              ARGMYQRWADLLSSESWQEVLDKTAAYQQEVMK
                                                                             YRGFYRAYQAHVSSSNWAEFEHASSTWHTELTK
                                                                                                              GPAGFLEQDDSENWCEIQKLLKGHRARNSKLCLEMGLGQEKRRDDGIPGIT-NYIFSETA
                                                                                                                                                                                                       RSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTI
                                                                                                                                                                                                                                            QDGHGSGFFFTEKPDANVWV--DGAVSSYYRETYAE---
                                                                                                                                                                                                                                                                        --PEGAGLOMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIY
                                                                                                                                                                                                                                                                                                          AEQFASDQYHALFSHASAVQVLGAKDDGSDKRLGD:
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                                                                                                                                                                                                                                                                                                                                                                        CVESYKGLIFGNWDTSAPGLRDYLGDIAWYLDGMLDRREGGTEIVGGVQKWVINCNWKFP
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Pred. No. 6e-51;
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                                                                              445
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A;Note: bphAlb
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Superfamily: toluene dioxygenase terminal oxygenase component large chain;
C;Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F;88,90,108,111/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
Ър
                                 Q
                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378399; PIDN:AAD03982.C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T31258
R; Romine, M.F.; Stillwell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aromatic oxygenase large chain - Sphingomonas aromaticivorans pl
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan_2000 #sequence_revision 11-Jan-2000 #text_change
                                                                                                                                                                                                                                         A; Genome: plasmid
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-455 <R
                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T31258
                                                                                Matches
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Best Local Similarity
11
                                        N
                       NYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGI 61
DYSRYMDLKEGWLDRR---IFSDADIYEEELYRIFARSWLFVAHESQIPSSGDFLTTHMGE
                                                                             Conservative
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                                                                                                30.1%;
36.1%;
                                                                             83;
                                                                         Score 725.5; DB 2;
Pred. No. 5e-50;
3; Mismatches 169;
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                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         E.C.; Sensen,
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83
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C.W.

#status

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A;Genome: plasmid

A;Genome: plasmid

C;Superfamily: toluene dioxygenase terminal oxygenase component large
C;Superfamily: toluene dioxygenase terminal oxygenase component large
C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; c
C;Keywords: 2Fe-2S; homology <RSK>
F;86-134/Domain: Rieske [2Fe-2S] homology <RSK>
F;96,98,116,119/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (cov
                                                                                                      g
                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain ML2 C;Comment: This enzyme is involved in catalyzing the oxidation of benzene to cisC;Comment: The reduced enzyme catalyzes the oxidation of benzene to cis-benzene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           benzene 1,2-dioxygenase (EC 1.14.12.3) terminal oxygenase component large chain C;Species: Pseudomonas putida C;Species: Pseudomonas putida C;Date: 19-May-1994 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000 C;Accession: JNOB12 R;Tan, H.M.; Tang, H.Y.; Joannou, C.L.; Abdel-Wahab, N.H.; Mason, J.R. Gene 130, 33-39, 1993
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A; Residues: 1-450 <TAN>
A; Cross-references: GB:L04642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The Pseudomonas putida ML2 plasmid-encoded genes for benzene dioxygenase A;Reference number: JN0810; MUID:93345820; PMID:8344526 A;Accession: JN0812
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                                                                                                        QCRHRGMRICRSDAGNAKAFTCSYHGWAYDTAGNLINVPYEAESFA
                                                                                                                                       VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
                                                                                                                                                                         IYTDEDLYQLELERVFARSWLLLGHETHIRKPGDYFTTYMGEDPVVVVRQKDASIAVFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFEMDDGENWENCTTVNRGVVTRHERLHYRCGIGRQIEHDTL-PGIVYRGQYNDANQRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SASIFPNVSFLPGISTFRQWQPKGPMQFELKTWVIVNKNMPDDIKEEVTKGVMQTFGPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMDNSYHASVNGHGWEFGTEGVGDLFLLGRPKVMDYYNKIRPKMAERLGEMRSKIFGSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QMTSKYGSGM-GVLWD-GYSGVHSADLV--PELMAFGGAKQERLNKEIGDVRARIYRSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFIGGCIKSVISANWKFGVENFIGDAYHAGWTHDSGTR-----SMNNGQPFPP----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYDAGDIDFKNHGLKNVAKVGNYKGLVFATFNSDAPSLEAWLGDFRWYLDMILDNEEGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVIVSRONDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                              27.18;
                                                                                                                                                                                                                                                                                                              2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:L04643; NID:g6552505;
                                                                                                                                                                                                                                                 69;
                                                                                                                                                                                                                                          Pred. No. 3.4e
); Mismatches
                                                                                                                                                                                                                                                                              Score 652.5;
                                                                                                                                                                                                                                                                No. 3.4e-44;
                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                               174;
                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:AAA17758.1; PID:g309855
                                                                                                        -CLDKKEWS
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                                  TASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSS
                                                                    PGINTVRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQDDGENWV
                                                                                                                                         GFYVGDPNLMLAIMGPKVTSYWTEGPASEKAAERLGSVERGSKLMVEHM--TVFPTCSFL
                                                                                                                                                                         VLWDGYSGVHSADLVPELMAF - -GGAKQERLNKEIGDVR - - ARIYRSHLNCTVFPNNSML
                                                                                                                                                                                                           WKFAAEQFCSDMYHAGTTSHLSGILAGLPEDL----EMADLAPPTVGKQYRASWGGHGS
                                                                                                                                                                                                                                             WKAPAENFVGDAYHVGWT-HASSLRSG--ESIFSSLAGNAALPPEGAGLQMTSKYGSGMG
                                                                                                                                                                                                                                                                              PLKARVETYKGLIFANWDENAVDLDTYLGEAKFYMDHMLDRTEAGTEAIPGVQKWVIPCN
                                                                                                                                                                                                                                                                                                                --VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKAN 194
                                                                                                                                                                                                                                                                                                                                                    QCRHRGMRICRADAGNAKAFTCSYHGWAYDTAGNLVNVPYEAESFA-----
                                                                                                                                                                                                                                                                                                                                                                                   VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE-- 137
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TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWESDDNDNME

381 367 321 307 263 251 IXTDEDLYQLELERVFARSWLLLGHETQIRKPGDYITTYMGEDPVVVVRQKDASIAVFLN

79

94

CLNKKEWS

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G;Superfamily: toluene dioxygenase terminal oxygenase component large chain; c;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; metalloprotein; oxidorec F;86-134/Domain; Rieske [ZFe-2S] homology <RSK> F;96,98,116,119/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
                                                                                                                                                                                                                                                                                           R:Zylstra, G.J.; Gibson, D.T.
J. Biol. Chem. 264, 14940-14946, 1989
A;Title: Toluene degradation by Pseudomonas
A;Reference number: A36516; MUID:89359301; i
A;Accession: A36516
                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Pseudomonas putida
C:Date: 15-Feb-1991 #sequence_revision
C:Accession: A36516
                                                                                                                                               A; Gene: todC1
C; Superfamily
                                                                                                                                                                                      A;Cross-references: GB:J04996; NID:g151600; A;Experimental source: strain F1 C;Genetics:
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-450 <ZYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                              toluene dioxygenase (EC 1.14.12.11) terminal oxygenase component large
                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
    145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHVSSSNW 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKFAAEQFCSDMYHAGTTAHLSGIIAGLPEDLELADLA--PP-----KFGKQYRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGENWVEIQHILRGHKARSRPFNAEMSMGQTVDNDPIYPGRISNNVYSEEAARGLYAHWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTCSFLPGVNTIRTWHPRGPNEVEVWAFTVVDADAPDDIKEEFRRQTLRTFSAGGVFEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGGHGSGFYIGDPNMMLAMMGPKVTSYLTEGPAAEKAAERLGSIERGTKIMLEHM--TVF
                          Similarity
  Conservative
                       27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LVPELMAF--GGAKQERLNKEIGDVR--ARIYRSHLNCTVF
71;
                     Score 650.5; DB 1
Pred. No. 4.9e-44;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       06-Jan-1995
                                                                                                                                                                                                                                                                                                                s putida F1. PMID:2670929
                                                                                                                                                                                                                                PIDN: AAA26005.1;
                                           DB 1;
    181;
                                                                                                                                                                                                                                                                                                                                                                                                                       #text_change
                                       Length
    Indels
                                                                                                                                                                                                                                                                                                                                        Nucleotide
                                                                                                                                                                                                                              PID:g15160;
                                             450;
    25;
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                                                                                                                                                                                                                                                                                                                                      sequence
  Gaps
                                                                                                                            e chain; Rieske oxidoreductase;
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                                                                                    #status
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S51757

S51757

Siphenyl dioxygenase (EC 1.14.-.-) large chain - Rhodococcus globerulus C; Species: Rhodococcus globerulus C; Species: Rhodococcus globerulus C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999 C; Accession: S51757

R; Asturlas, J.A.; Diaz, E.; Timmis, K.N.

R; Baturlas, J.A.; Diaz, Library, July 1994

A; Description: Evolutionary relationship of the biphenyl dioxygenase of the
RESULT
B41858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: toluene dioxygenase terminal oxygenase component large chain; Rieske [;C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein F;89-137/Domain: Rieske [2Fe-2S] homology <RSK>F;99,101,119,122/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status
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A; Residues: 1-461 <AST>
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Best Local
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                                                                                                                                                                                                                 APDWAALNATRPTPNADVS
                                                                                                                                                                                                                                                      SSNWAEFEHASSTWHTELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHGSGFYIGEMGTLAAVMGMKILEYYTSGPAAEKAAKRLGSAVRGSQATGQHMTVFPTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAENFVGDAYHVGWT-HASSLRSGESIFSSLAGNAALP------PEGAGLQMTSKYG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMF-KHSGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCRHRGMRICRADGGNAKSFTCSYHGWAYDSAGNLVSVPFQQEAFPD-LKKEDWGPLK-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DW 443
                                                                                                                                                                                                                                                                                            WVEIQSVLRGHKARSRPFNAEMSLREINTADPDWPGTI-SYVYSEEAARGFYAHWSRMMT
                                                                                                                                                                                                                                                                                                                                METASONGKKYOSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVS 425
                                                                                                                                                                                                                                                                                                                                                                     FLPGINTIRTWHPRGPHEIEVWSFTVVDADAPAEIKEEYRRQTIRTFSAGGVFDQDDGEN
                                                                                                                                                                                                                                                                                                                                                                                                         MLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWESDDNDN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAEQFCSDMYHVGTTSHLSGLLAG------LPDEIDIREVQPPTTGIQYSAPWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARVETYKGLIFANWDSEAPDLDTYLGEAKFYMDHMLDRTEAGTEALPGIEKWVIQCNWKF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLG-LKEV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .. ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGMGVLWDGYSGVHSADLVPELMAF---GGAKQERLNKEIGDVRARIYRSHLNCTVFPNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYTDEALYQQELELIFGRSWLLLGHETQIPKAGDFMTQYMGEDPVIVSRQRDGSISVFLN
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33.7%;
                                                                                                                                                                                                                                                      444
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; Pred. No. 4.2e-43;
74; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID: g607171; PIDN: CAA56346.1;
transcriptional mapping of the genes encoding bipheny
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                                                                                                                 component large chain
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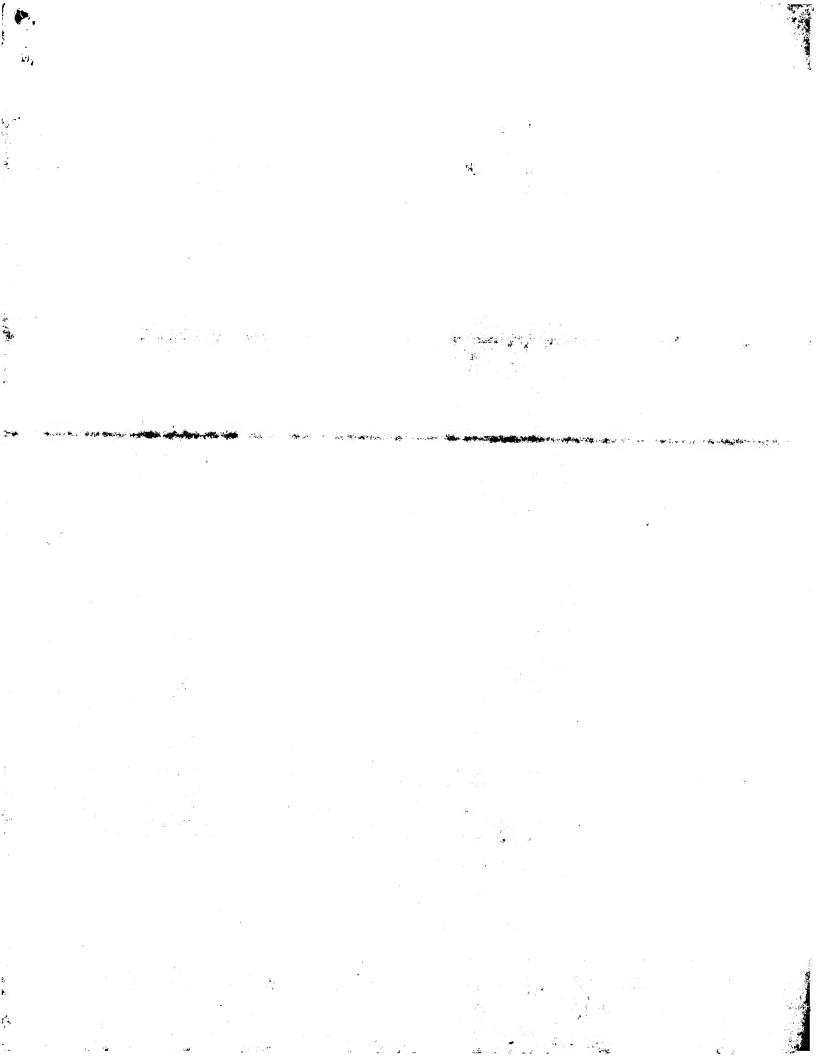
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A; Residues: 1-459 < ERI>
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                                          AIGETSYRGFYRAYQAHVSSSNWA 430
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Run on:
                                                                                                                 OM protein - protein search, using sw model
January 27, 2003, 08:46:47; Search time 29.1667 Seconds (without alignments) 2051.298 Million cell updates/sec
                                                                                                                                                                                                        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Title: Perfect score: US-09-843-250-36 2408 1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

908470 seqs, 133250620 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Naphthalene	AAB12583	21		99.7	2401	10
AAB12580 Naphthalene dioxyg	AAB12580	21	449	99.8	2403	ာထာ
Naphthalene	AAB12579	21		99.8	2403	7
Naphthalene Naphthalene	AAB12577	21		99.8	2404	م ر
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NDO related	AAB12566	21		100.0	2407	ω
AAB12565 Naphthalene dioxyq	AAB12565	21		100.0	2407	2
	AAB12582	21		100.0	2408	1
ID Description	IJ	DB	Query Match Length	Query	Score	Result No.

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AAW80332	AAW79020	AAW79019	AAW79018	ABG18089	ABB93163	ABP35375	AAW69562	AAW69563	ABB06798	AAG62635	AAG62633	AAG62634	AAU33601	AAB79227	AAU36099	AAG92386	AAR32085	AAY81989	AAY81990	AAR66729	AA017350	AAY83939	AAU34660	AAB29474	AAB12576	AAB12575	AAB12574	AAB12573	AAB12572	AAB12571	AAB12570	9	AAB12584	AAB12578
e amino ac	motif in	motif in	motif	Novel human diagno	Herbicidally activ	Human oxygenase-li	Spinach choline mo	Sugarbeet choline	Atriplex hortensis	C album choline mo	album choline		Pseudomonas aerugi	Corynebacterium gl	Klebsiella pneumon	C glutamicum prote	Benzene dioxygenas		Chimeric PCB decom		cter	ring hydr	E. coli cellular p	Burkholderia sp. C	related	related		related	related	related	related		Naphthalene dioxyg	Naphthalene dioxyg

ALIGNMENTS

09-NOV-2000 AAB12582; AAB12582 standard; Protein; 449 Naphthalene dioxygenase mutant F352I protein sequence SEQ ID NO:36. (first entry) Ą

Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral diol; polymer; resin; pharmaceutical; rubber industry; bioremediation.

Pseudomonas sp Synthetic.

WO200037480-A1

26-OCT-1999; 29-JUN-2000 99WO-US25079

26-OCT-1998;

98US-0105575

(IOWA) UNIV IOWA RES FOUND.

Parales R, Gibson Ď Resnick Ś Lee

WPI; 2000-452174/39. N-PSDB; AAA65356.

Novel naphthalene dioxygenase mutant having a specific amino acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a naphthalene dioxygenase (NDO) or NDO CC related complex (I) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific CC positions. The polypeptides and host cells are useful for preparing CC (-)-(15, 2R)-cis-paththalene dihydroidol, (- or +)-cis-biphenyl-3,4-CC dihydroxylndan, 1,2-dihydroxxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC dihydroxylndan, 2-dihydronaphthalene, respectively. The polypeptides and CC the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,3-dihydroxy-3,4-dihydroxy-3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,3-dihydroxy-1,3-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which constant compound such as indene, 1,2-dihydrophenanthrene and CC benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzoltane, contacting them with phenanthrene, dibenzoltane, cc dibenzothiophene, 9,10-dihydroanthracene, dibenzoltane, phenanthrene and CC corresponding dihydro dihydroanthracene, or 9,10-dihydrophenanthrene and CC corresponding dihydro dihydroanthracene, or 9,10-dihydrophenanthrene and CC corresponding dihydro dihydroanthracene, or 9,10-dihydrophenanthrene and CC cells are useful for preparing chiral diols for use in the polymer. CC cells are useful for preparing chiral diols for use in the polymer of the present sequence represents constitution of the polymer invention.
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AAB12565
                                      AAB12565 standard;
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                                                                                                                                                                                                                                                                                                        FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                        449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2408;
Pred. No. 1.2
0; Mismatches
                                                                                                                                         449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
1.2e-224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local
                                                                                                                                    Matches
                                                                                                                                                                                                                                                  benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, dibenzofuran, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the
                                                                                                                                                                                                                                                                                                                                                                      involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel naphthalene dioxygenase mutant having a specific substitution for preparing chiral diols for use in the pharmaceutical or rubber industry and for carrying out
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                      exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parales R, Gibson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200037480-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inducible multi-component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Naphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymer; resin;
61
                                 61
                                                                                     1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a naphthalene dioxygenase
                                                                  MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                    cal Similarity
448; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-452174/39
DB; AAA65339.
IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 58-60; 151pp;
                                                                                                                                                                                                        449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dioxygenase mutant F352V
                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain NCIB 9816-4; naphthalene dioxygenase; NDO; component enzyme; alpha subunit; mutant; chiral d pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                      the
                                                                                                                                                100.0%;
                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Resnick
                                                                                                                                  Pred. No. 1.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                 e 2407; DB 21;
No. 1.5e-224;
smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                    Indels
                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chiral diol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NDO)
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Qy

121

KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL

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RESULT 3
AAB12566
ID AAB1
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The present invention describes a naphthalene dioxygenase (NDO) or NDO related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (')-(1S,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (1S,2R)-cis-phenanthrene-1,2-dihydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2,cdihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 99-100; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1998;
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                                                                                                                                                                                                                                      Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDC inducible multi-component enzyme; alpha subunit; mutant; chiral polymer; resin; pharmaceutical; rubber industry; bioremediation.
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resin; pharmaceutical; ru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes a naphthalene dioxygenase (NDO) or plex (I) comprising several polypeptides which contain
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Best Local Si Matches 448; Query Match

Similarity

99.9%;

Score 2406; D Pred. No. 1.8e 1; Mismatches

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Length Indels

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Conservative

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                     Disclosure;
                                               Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                           Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral diol; polymer; resin; pharmaceutical; rubber industry; bioremediation.
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                                                                                                                          Parales R, Gibson D,
                                                                                                                                                                    26-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                    dioxygenase alpha subunit protein sequence
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                    118-120;
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The

present

invention

describes

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naphthalene

dioxygenase

(NDO)

or

NDC

Pseudomonas sp.

Naphthalene dioxygenase mutant F352A protein sequence

SEQ ID

NO: 33

inducible multi-component enzyme; alpha subunit; mutant; chiral diol

strain NCIB 9816-4; naphthalene dioxygenase;

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RESULT 7
AAB12579
ID AAB1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15.2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15.2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
                                                                                  09-NOV-2000
                                                                                                                                                    AAB12579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9816-4, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related complex (I) comprising several polypeptides which contain
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                                                                                                                                                    standard;
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                                                                                  (first entry)
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alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-) (1s,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-3C dihydrodiol, (1s,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-3.4-3C dihydrodiol, (1s,2R)-cis-phenanthrene, biphenyl, phenanthrene, which compounds them with naphthalene, biphenyl, phenanthrene, cidhydroxy-1,2,3,4-tetrahydronaphthalene, which contacting them with naphthalene, biphenyl, phenanthrene, which contacting them with phenanthrene. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxphenanthrene or 3,4-dihydroxy-3,4-dihydroxphenanthrene which convolves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, and thracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, caenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, acenaphthylene, preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, cells are useful for preparing chiral diols for use in the polymer, an aphthalene dioxygenase (NDO) mutant alpha subunit, given in the caenaphthy and the presents are constituted in the present sequence represents and the polymer, and the present sequence represents and the polymer presents and the present invention.
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(-)-(15,2R)-cis-naphthalene dihydrodiol, (-or+)-cis-biphenyl-3,4-cis-dihydroxylindan, (15,2R)-cis-phenanthrene-1,2-dihydroxylindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, cindene, and 1,2-dihydroxpaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-1,2-cidhydroxy-
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Matches 448;
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                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                     09-NOV-2000
                                                                                                                                                                                                                                                                                                                    AAB12568 standard;
                                  (IOWA ) UNIV IOWA RES
                                                                                                                                                                                             polymer;
                                                                                                                                                                                                                                             NDO related
                                                                                                                                                                                                                                                                                               AAB12568;
                                                            26-OCT-1998;
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                                                                                                                                                                                                          Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d
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Query Match Best Local Matches 447;

Local Similarity

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Length 449; Indels

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CC (-)-(15,2R)-(15-napththalene dihydrodiol, (-0 r+)-(15-biphenayl-3,4-CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydroxnaphthalene, which CC dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which CC involves contacting them with naphthalene, biphenyl, phenanthrene, CC indene, and 1,2-dihydroxnaphthalene respectively. The polypeptides and CC the host cells are also useful for preparing 1,2-dihydroxy 1,2-CC dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-CC dihydrophenanthrene which CC host cells are also used in bioremediation in which they oxidise an CC aromatic compound such as indene, 1,2-dihydronaphthalene, compound such as indene, biphenyl, fluorene, dibenzofuran, compound such as indene, biph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a naphthalene dioxygenase (NDO) or a related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
Sequence
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449 AA;
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                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
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Pred. No. 4.5e-224;
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                                                                                                                                                                                                                                                 The present invention describes a naphthalene dioxygenase (NDO) or NDO Crelated complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-naphthalene dihydrodiol, (- or +)-cis-biphenyl-3,4-Cidhydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-Cidhydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, which host cells are also useful for preparing 1,2-dihydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-3,4-dihydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-3,4-dihydroxy-1,2-Cidhydroxy-3,4-dihydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhydroxy-1,2-Cidhy
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                                                                                                                                                                                                                    Sequence
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DB; AAA65376.
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                                                                                                                               Conservative
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                                                                                                                                                   99.78;
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                                                                                                                                                   Score 2401; DB 21; Pred. No. 5.6e-224;
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e; alpha subunit; mutant; chiral
rubber industry; bioremediation.
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                                                                                                                                     Length
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bioremediation
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                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                   pharmaceutical or
                                                                                                                                         Novel naphthalene
                                                                                                                                                                                                                                                                                                          WO200037480-A1
                                                                                                                                substitution
                                                                                                                                                                                               Parales
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                                                                                                                                                                                                                                                                                                                                          Pseudomonas
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                                                                                                                                                                AAA65352
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                                                                                                                                                                                              Gibson D,
                                                                                                                 alene dioxygenase mutant having a specific
for preparing chiral diols for use in the
al or rubber industry and for carrying out
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The present invention describes a naphthalene dioxygenase (NDO) or N related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted actions at specific positions. The polypeptides and host cells are useful for preparing (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydrodiol, cis-1,2-dihydrodiol

Claim

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Page 126-127; 151pp;

English

or NDO

dihydroxyindan,

1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an
                                                                       Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral d polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                     09-NOV-2000
                                                                                                                                                                                                                                  AAB12584 standard;
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                                           Pseudomonas
                                                                                                                                    Naphthalene dioxygenase mutant F352Y protein sequence SEQ
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                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                  Protein;
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cc involves contacting them with naphthalene, biphenyl, phenanthrene, contacting them with naphthalene, biphenyl, phenanthrene, cc indene, and 1,2-dihydronaphthalene respectively. The polypeptides and ct the host cells are also useful for preparing 1,2-dihydroxy-1,2-cc dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which convolves contacting them with phenanthrene. The polypeptides and the classific compound such as indene, 1,2-dihydrophenanthrene which they oxidise an cc aromatic compound such as indene, 1,2-dihydronaphthalene, cc benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, cc acenaphthylene, naphthalene, biphenyl, fluorene, dibenzofuran, cc dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cc cells are useful for preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the cc exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                  alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(15.2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (15.2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
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N-PSDB; AAA65377.
Sequence
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448 AA;
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                                                                                                                                                                                                                                                        IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTYGPAGFWES
                                                         QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                       QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                   ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                               ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                            KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                                                                                                  MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                                                                                                                                                                                       IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                         99.6%;
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                           Score 2398; DB 21;
Pred. No. 1.1e-223;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                       Length 448;
                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                           180
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                                                                                                                   240
                                                                                                                                               240
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Query Match Best Local Similarity

99.5%; 99.3%;

Score 2397; Pred. No. 1

Length 449;

0;

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RESULT 13
AAB12569
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                                             involves contacting them with phenanthrene. The polypeptides and the host cells are also used in bioremediation in which they oxidise an aromatic compound such as indene, 1,2-dihydronaphthalene, benzocyclohelpt-1-ene, anthracene, phenanthrene, dibenzo(1,4)dioxan, acenaphthylene, naphthalene, biphenyl, fluorene, dibenzo(1,4)dioxan, dibenzothiophene, 9,10-dihydroanthracene, or 9,10-dihydrophenanthrene a corresponding dihydro dihydroxy compound. The polypeptides and the host cells are useful for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry. The present sequence represent a naphthalene dioxygenase (NDO) mutant alpha subunit, given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                related complex (I) comprising several polypeptides which contain an alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing (-)-(IS,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-dihydrodiol, (IS,2R)-cis-phenanthrene-1,2-dihydrodiol, cis-1,2-dihydroxyindan, 1,2-dihydroxy-1,2,3,4-tetrahydronaphthalene, which involves contacting them with naphthalene, biphenyl, phenanthrene, indene, and 1,2-dihydronaphthalene respectively. The polypeptides and the host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-3,4-dihydrophenanthrene which host cells are which host cells are also useful for preparing 1,2-dihydroxy-1,2-dihydrophenanthrene or 3,4-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-dihydroxy-1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin, pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-452174/39.
N-PSDB; AAA65343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inducible multi-component enzyme; alpha subunit; mutant; chiral
polymer; resin; pharmaceutical; rubber industry; bioremediation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDO related complex alpha subunit protein sequence SEQ ID NO:17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 104-105; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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RESULT 14
AAB12570
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Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, repharmaceutical or rubber industry and for carrying out bloremedia
                                                                                                                    (IOWA ) UNIV IOWA
                                                                                                                                                                                                                                                                                         Pseudomonas sp. strain NCIB 9816-4; naphthalene dioxygenase; NDO; inducible multi-component enzyme; alpha subunit; mutant; chiral c polymer; resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                AAB12570;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB12570 standard; Protein; 449
                                                       N-PSDB;
                                                                                                                                                 26-OCT-1998;
                                                                                                                                                                         26-OCT-1999;
                                                                                                                                                                                                   29-JUN-2000
                                                                                                                                                                                                                            WO200037480-A1
                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                  Pseudomonas
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                                                                   2000-452174/39
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                                                                                                                                                                                                                                                                                                                                              complex alpha subunit protein sequence
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                                                                                             Resnick
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1.4e-223;
                                                                                                                                                                                                                                                                                                                                               SEQ ID
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polymer, resin bioremediation

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RESULT 15
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Best Local S
Matches 434
                                        AAB12571;
                                                                                AAB12571 standard; Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha subunit that contains substituted amino acids at specific positions. The polypeptides and host cells are useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                          421
                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (-)-(18,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3,4-
                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes a naphthalene dioxygenase (NDO) or Nated complex (I) comprising several polypeptides which contain an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG 60
                                                                                                                                                                                                                                                                                                                                                                                 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
                                                                                                                                                                                       QAHVSSSNWAEFEDASSTWHTELTKTTDR
                                                                                                                                                                                                            QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                          DDNDNMETASQNGKKYQSRDSDLLSNLGFGKDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPIFKHSGGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                   DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGSKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDEVIYSRQNDGSIRAFLNVCRHRGKTLYSVEAGNAKGFYCSYHGWGFGSNGELQSVPFE 120
                                                                                                                                                                                                                                                                                                                                                             FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFASLAGNAVLPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Page 105-107; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 2349; DB 21; 96.7%; Pred. No. 6.3e-219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NDO) or NDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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09-NOV-2000

(first entry)

В Qy

61 61

IDEVIVSRQSDGSIRAFLNVCRHRGKTLVNAEAGNAKGFVCSYHGWGFGSNGELQSVPFE IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120

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ДЪ
                                                                                                                                         CC related complex (I) comprising several polypeptides which contain an CC alpha subunit that contains substituted amino acids at specific cpositions. The polypeptides and host cells are useful for preparing CC (-)-(15,2R)-cis-napththalene dihydrodiol, (- or +)-cis-biphenyl-3.4-CC dihydroxyindan, 1,2-dihydroxyl-1,2-3,4-tetrahydronaphthalene, which cis-leves contacting them with naphthalene, biphenyl, phenanthrene, which college, and 1,2-dihydronaphthalene respectively. The polypeptides and college, and 1,2-dihydronaphthalene respectively. The polypeptides and college, and 1,2-dihydronaphthalene respectively. The polypeptides and college, and 1,2-dihydronaphthalene, and 1,2-dihydrophenanthrene which college contacting them with phenanthrene. The polypeptides and the college contacting them with phenanthrene. The polypeptides and the college contacting them with phenanthrene. The polypeptides and the constitution of the polypeptides and the corresponding dihydro dihydroanthracene, of 1,0-dihydronaphthalene, dibenzo(1,4)dioxan, constitution of the preparing chiral diols for use in the polymer, cresin, pharmaceutical or rubber industry. The present sequence represents anaphthalene dioxygenase (NDO) mutant alpha subunit, given in the company of the present invention.
                                                                     Matches
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel naphthalene dioxygenase mutant having a specific amino acid substitution for preparing chiral diols for use in the polymer, resin pharmaceutical or rubber industry and for carrying out bioremediation
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 107-109; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-452174/39
N-PSDB; AAA65345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parales R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200037480-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDO related complex alpha subunit protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inducible multi-component
                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes a naphthalene dioxygenase (NDO) or NDO
                                  MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
                                                                     al Similarity
429; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e multi-component enzyme; alpha subunit; mutant; chiral
resin; pharmaceutical; rubber industry; bioremediation.
                                                                                                                                       449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibson D,
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "unspecified"
                                                                                    96.4%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Resnick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9816-4;
                                                                 Score 2321; DB 21;
Pred. No. 3.3e-216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        naphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dioxygenase;
                                                                                                    Length
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO:19
                                                                                                      449;
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